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(54) Title: NEISSERIA MENINGITIDIS ANTIGENS			
(57) Abstract			
<p>The invention provides proteins from <i>Neisseria meningitidis</i> (strains A and B), including amino acid sequences, the corresponding nucleotide sequences, expression data, and serological data. The proteins are useful antigens for vaccines, immunogenic compositions, and/or diagnostics.</p>			

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NEISSERIA MENINGITIDIS ANTIGENS

This invention relates to antigens from the bacterium *Neisseria meningitidis*.

BACKGROUND

Neisseria meningitidis is a non-motile, gram negative diplococcus human pathogen. It colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. It is closely related to *N.gonorrhoeae*, although one feature that clearly differentiates meningococcus from gonococcus is the presence of a polysaccharide capsule that is present in all pathogenic meningococci.

N.meningitidis causes both endemic and epidemic disease. In the United States the attack rate is 0.6-1 per 100,000 persons per year, and it can be much greater during outbreaks (see Lieberman *et al.* (1996) Safety and Immunogenicity of a Serogroups A/C *Neisseria meningitidis* Oligosaccharide-Protein Conjugate Vaccine in Young Children. *JAMA* 275(19):1499-1503; Schuchat *et al* (1997) Bacterial Meningitis in the United States in 1995. *N Engl J Med* 337(14):970-976). In developing countries, endemic disease rates are much higher and during epidemics incidence rates can reach 500 cases per 100,000 persons per year. Mortality is extremely high, at 10-20% in the United States, and much higher in developing countries. Following the introduction of the conjugate vaccine against *Haemophilus influenzae*, *N. meningitidis* is the major cause of bacterial meningitis at all ages in the United States (Schuchat *et al* (1997) *supra*).

Based on the organism's capsular polysaccharide, 12 serogroups of *N.meningitidis* have been identified. Group A is the pathogen most often implicated in epidemic disease in sub-Saharan Africa. Serogroups B and C are responsible for the vast majority of cases in the United States and in most developed countries. Serogroups W135 and Y are responsible for the rest of the cases in the United States and developed countries. The meningococcal vaccine currently in use is a tetravalent polysaccharide vaccine composed of serogroups A, C, Y and W135. Although efficacious in adolescents and adults, it induces a poor immune response and short duration of protection, and cannot be used in infants [eg. Morbidity and Mortality weekly report, Vol.46, No. RR-5 (1997)]. This is because polysaccharides are T-cell independent antigens that induce a weak immune response that cannot be boosted by repeated immunization. Following the success of the

vaccination against *H.influenzae*, conjugate vaccines against serogroups A and C have been developed and are at the final stage of clinical testing (Zollinger WD "New and Improved Vaccines Against Meningococcal Disease" in: *New Generation Vaccines, supra*, pp. 469-488; Lieberman *et al* (1996) *supra*; Costantino *et al* (1992) Development and phase I clinical testing of a conjugate vaccine against meningococcus A and C. *Vaccine* 10:691-698).

Meningococcus B remains a problem, however. This serotype currently is responsible for approximately 50% of total meningitis in the United States, Europe, and South America. The polysaccharide approach cannot be used because the menB capsular polysaccharide is a polymer of $\alpha(2-8)$ -linked *N*-acetyl neuraminic acid that is also present in mammalian tissue. This results in tolerance to the antigen; indeed, if an immune response were elicited, it would be anti-self, and therefore undesirable. In order to avoid induction of autoimmunity and to induce a protective immune response, the capsular polysaccharide has, for instance, been chemically modified substituting the *N*-acetyl groups with *N*-propionyl groups, leaving the specific antigenicity unaltered (Romero & Outschoorn (1994) Current status of Meningococcal group B vaccine candidates: capsular or non-capsular? *Clin Microbiol Rev* 7(4):559-575).

Alternative approaches to menB vaccines have used complex mixtures of outer membrane proteins (OMPs), containing either the OMPs alone, or OMPs enriched in porins, or deleted of the class 4 OMPs that are believed to induce antibodies that block bactericidal activity. This approach produces vaccines that are not well characterized. They are able to protect against the homologous strain, but are not effective at large where there are many antigenic variants of the outer membrane proteins. To overcome the antigenic variability, multivalent vaccines containing up to nine different porins have been constructed (*eg.* Poolman JT (1992) Development of a meningococcal vaccine. *Infect. Agents Dis.* 4:13-28). Additional proteins to be used in outer membrane vaccines have been the opa and opc proteins, but none of these approaches have been able to overcome the antigenic variability (*eg.* Ala'Aldeen & Borriello (1996) The meningococcal transferrin-binding proteins 1 and 2 are both surface exposed and generate bactericidal antibodies capable of killing homologous and heterologous strains. *Vaccine* 14(1):49-53).

A certain amount of sequence data is available for meningococcal and gonococcal genes and proteins (*eg.* EP-A-0467714, WO96/29412), but this is by no means complete. The provision of further sequences could provide an opportunity to identify secreted or surface-exposed proteins that

are presumed targets for the immune system and which are not antigenically variable. For instance, some of the identified proteins could be components of efficacious vaccines against meningococcus B, some could be components of vaccines against all meningococcal serotypes, and others could be components of vaccines against all pathogenic *Neisseriae*.

5 THE INVENTION

The invention provides proteins comprising the *N.meningitidis* amino acid sequences disclosed in the examples.

It also provides proteins comprising sequences homologous (*ie.* having sequence identity) to the *N.meningitidis* amino acid sequences disclosed in the examples. Depending on the particular
10 sequence, the degree of sequence identity is preferably greater than 50% (*eg.* 60%, 70%, 80%, 90%, 95%, 99% or more). These homologous proteins include mutants and allelic variants of the sequences disclosed in the examples. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between the proteins is preferably determined by the Smith-Waterman homology search algorithm as implemented in the MPSRCH
15 program (Oxford Molecular), using an affine gap search with parameters *gap open penalty=12* and *gap extension penalty=1*.

The invention further provides proteins comprising fragments of the *N.meningitidis* amino acid sequences disclosed in the examples. The fragments should comprise at least *n* consecutive amino acids from the sequences and, depending on the particular sequence, *n* is 7 or more (*eg.* 8, 10, 12,
20 14, 16, 18, 20 or more). Preferably the fragments comprise an epitope from the sequence.

The proteins of the invention can, of course, be prepared by various means (*eg.* recombinant expression, purification from cell culture, chemical synthesis *etc.*) and in various forms (*eg.* native, fusions *etc.*). They are preferably prepared in substantially pure form (*ie.* substantially free from other *N.meningitidis* or host cell proteins)

25 According to a further aspect, the invention provides antibodies which bind to these proteins. These may be polyclonal or monoclonal and may be produced by any suitable means.

According to a further aspect, the invention provides nucleic acid comprising the *N.meningitidis* nucleotide sequences disclosed in the examples. In addition, the invention provides nucleic acid comprising sequences homologous (*ie.* having sequence identity) to the *N.meningitidis* nucleotide sequences disclosed in the examples.

- 5 Furthermore, the invention provides nucleic acid which can hybridise to the *N.meningitidis* nucleic acid disclosed in the examples, preferably under "high stringency" conditions (*eg.* 65°C in a 0.1xSSC, 0.5% SDS solution).

Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least *n* consecutive nucleotides from the *N.meningitidis* sequences and, depending on the
10 particular sequence, *n* is 10 or more (*eg.* 12, 14, 15, 18, 20, 25, 30, 35, 40 or more).

According to a further aspect, the invention provides nucleic acid encoding the proteins and protein fragments of the invention.

It should also be appreciated that the invention provides nucleic acid comprising sequences complementary to those described above (*eg.* for antisense or probing purposes).

- 15 Nucleic acid according to the invention can, of course, be prepared in many ways (*eg.* by chemical synthesis, from genomic or cDNA libraries, from the organism itself *etc.*) and can take various forms (*eg.* single stranded, double stranded, vectors, probes *etc.*).

In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also peptide nucleic acids (PNA) *etc.*

- 20 According to a further aspect, the invention provides vectors comprising nucleotide sequences of the invention (*eg.* expression vectors) and host cells transformed with such vectors.

According to a further aspect, the invention provides compositions comprising protein, antibody, and/or nucleic acid according to the invention. These compositions may be suitable as vaccines, for instance, or as diagnostic reagents, or as immunogenic compositions.

The invention also provides nucleic acid, protein, or antibody according to the invention for use as medicaments (eg. as vaccines) or as diagnostic reagents. It also provides the use of nucleic acid, protein, or antibody according to the invention in the manufacture of: (i) a medicament for treating or preventing infection due to Neisserial bacteria; (ii) a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria; and/or (iii) a reagent which can raise antibodies against Neisserial bacteria. Said Neisserial bacteria may be any species or strain (such as *N.gonorrhoeae*) but are preferably *N.meningitidis*, especially strain A, strain B or strain C.

The invention also provides a method of treating a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid, protein, and/or antibody according to the invention.

According to further aspects, the invention provides various processes.

A process for producing proteins of the invention is provided, comprising the step of culturing a host cell according to the invention under conditions which induce protein expression.

A process for producing protein or nucleic acid of the invention is provided, wherein the protein or nucleic acid is synthesised in part or in whole using chemical means.

A process for detecting polynucleotides of the invention is provided, comprising the steps of: (a) contacting a nucleic probe according to the invention with a biological sample under hybridizing conditions to form duplexes; and (b) detecting said duplexes.

A process for detecting proteins of the invention is provided, comprising the steps of: (a) contacting an antibody according to the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

Unlike the sequences disclosed in PCT/IB98/01665, the sequences disclosed in the present application are believed not to have any significant homologs in *N.gonorrhoeae*. Accordingly, the sequences of the present invention also find use in the preparation of reagents for distinguishing between *N.meningitidis* and *N.gonorrhoeae*

A summary of standard techniques and procedures which may be employed in order to perform the invention (eg. to utilise the disclosed sequences for vaccination or diagnostic purposes) follows. This summary is not a limitation on the invention but, rather, gives examples that may be used, but are not required.

5 General

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature eg. Sambrook *Molecular Cloning; A Laboratory Manual, Second Edition* (1989); *DNA Cloning, Volumes I and*
10 *ii* (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); *Transcription and Translation* (B.D. Hames & S.J. Higgins eds. 1984); *Animal Cell Culture* (R.I. Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene*
15 *Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D.M. Weir and C. C. Blackwell eds 1986).

20 Standard abbreviations for nucleotides and amino acids are used in this specification.

All publications, patents, and patent applications cited herein are incorporated in full by reference. In particular, the contents of UK patent applications 9800760.2, 9819015.0 and 9822143.5 are incorporated herein.

Definitions

25 A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

The term "comprising" means "including" as well as "consisting" *eg.* a composition "comprising" X may consist exclusively of X or may include something additional to X, such as X+Y.

The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the
5 heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a Neisserial sequence is heterologous to a mouse host cell. A further examples would be two epitopes from the same or different proteins which have been assembled in a single protein in an arrangement not found in nature.

10 An "origin of replication" is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to replicate in a particular host cell. With certain
15 origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

A "mutant" sequence is defined as DNA, RNA or amino acid sequence differing from but having sequence identity with the native or disclosed sequence. Depending on the particular sequence, the
20 degree of sequence identity between the native or disclosed sequence and the mutant sequence is preferably greater than 50% (*eg.* 60%, 70%, 80%, 90%, 95%, 99% or more, calculated using the Smith-Waterman algorithm as described above). As used herein, an "allelic variant" of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs essentially at the same locus in the genome of another or second
25 isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions (*eg.* see US patent 5,753,235).

Expression systems

The Neisserial nucleotide sequences can be expressed in a variety of different expression systems; for example those used with mammalian cells, baculoviruses, plants, bacteria, and yeast.

i. Mammalian Systems

5 Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (eg. structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription
10 initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation [Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells." In *Molecular Cloning: A*
15 *Laboratory Manual*, 2nd ed.].

Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-
20 viral genes, such as the murine metallothionein gene, also provide useful promoter sequences. Expression may be either constitutive or regulated (inducible), depending on the promoter can be induced with glucocorticoid in hormone-responsive cells.

The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a regulatory DNA sequence that can
25 stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter [Maniatis et al. (1987) *Science* 236:1237; Alberts et al. (1989) *Molecular Biology of the Cell*, 2nd ed.]. Enhancer elements
30 derived from viruses may be particularly useful, because they usually have a broader host range.

Examples include the SV40 early gene enhancer [Dijkema et al (1985) *EMBO J.* 4:761] and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus [Gorman et al. (1982b) *Proc. Natl. Acad. Sci.* 79:6777] and from human cytomegalovirus [Boshart et al. (1985) *Cell* 41:521]. Additionally, some enhancers are regulatable and become active only
5 in the presence of an inducer, such as a hormone or metal ion [Sassone-Corsi and Borelli (1986) *Trends Genet.* 2:215; Maniatis et al. (1987) *Science* 236:1237].

A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired,
10 the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo*
15 or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus tripartite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

Usually, transcription termination and polyadenylation sequences recognized by mammalian cells
20 are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation [Birnstiel et al. (1985) *Cell* 41:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B.D. Hames and D.M. Glover); Proudfoot (1989) *Trends Biochem.*
25 *Sci.* 14:105]. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator/polyadenylation signals include those derived from SV40 [Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*].

Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers, introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (eg. plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 [Gluzman (1981) *Cell* 23:175] or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replication systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 [Kaufman et al. (1989) *Mol. Cell. Biol.* 9:946] and pHEBO [Shimizu et al. (1986) *Mol. Cell. Biol.* 6:1074].

The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (eg. Hep G2), and a number of other cell lines.

ii. Baculovirus Systems

The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the components of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus

genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

- 5 After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *inter alia*, Invitrogen, San Diego CA ("MaxBac" kit).
- 10 These techniques are generally known to those skilled in the art and fully described in Summers and Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987) (hereinafter "Summers and Smith").

Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and

15 transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This construct may contain a single gene and operably linked regulatory elements; multiple genes, each with its owned set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extrachromosomal element (*eg.* plasmids) capable of stable

20 maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and

25 which introduces a BamHI cloning site 32 basepairs downstream from the ATT; see Luckow and Summers, *Virology* (1989) 17:31.

The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.*, 42:177) and a prokaryotic ampicillin-resistance (*amp*) gene and origin of replication for selection and propagation in *E. coli*.

Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3') transcription of a coding sequence (eg. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding
5 sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly
10 useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlak et al., (1988), *J. Gen. Virol.* 69:765.

DNA encoding suitable signal sequences can be derived from genes for secreted insect or
15 baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene*, 73:409). Alternatively, since the signals for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as
20 those derived from genes encoding human α -interferon, Maeda et al., (1985), *Nature* 315:592; human gastrin-releasing peptide, Lebacqz-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA*, 82:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* 58:273; and human glucocerebrosidase, Martin et al. (1988) *DNA*, 7:99, can also be used to provide for secretion in insects.

25 A recombinant polypeptide or polyprotein may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by *in vitro* incubation with
30 cyanogen bromide.

Alternatively, recombinant polyproteins or proteins which are not naturally secreted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus -- usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. (See Summers and Smith *supra*; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) 3:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* 4:91. The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.

The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between about 1% and about 5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuclei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15 μm in size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus) or absence (indicative of recombinant

virus) of occlusion bodies. "Current Protocols in Microbiology" Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers and Smith, *supra*; Miller et al. (1989).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, *inter alia*: *Aedes aegypti*, *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni* (WO 89/046699; Carbonell et al., (1985) *J. Virol.* 56:153; Wright (1986) *Nature* 321:718; Smith et al., (1983) *Mol. Cell. Biol.* 3:2156; and see generally, Fraser, *et al.* (1989) *In Vitro Cell. Dev. Biol.* 25:225).

Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. *See, eg.* Summers and Smith *supra*.

The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible control, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the product of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, *eg.* HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, or the like. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also secreted in the medium or result from lysis of insect cells, so as to provide a product which is at least substantially free of host debris, *eg.* proteins, lipids and polysaccharides.

In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

iii. Plant Systems

There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as:

US 5,693,506; US 5,659,122; and US 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987); Whittier et al., *Nucleic Acids Research* 15:2515-2535 (1987); Wirsal et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R.L. Jones and J. MacMillin, *Gibberellins*: in: *Advanced Plant Physiology*, Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell*, 2:1027-1038(1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci.* 84:1337-1339 (1987)

Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker; and, for *Agrobacterium* transformations, T DNA sequences for *Agrobacterium*-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a selectable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilmink and Dons, 1993, *Plant Mol. Biol. Repr.*, 11(2):165-185.

Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward

antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

A heterologous coding sequence may be for any protein relating to the present invention. The sequence encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the cells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet.*, 202:179-185, 1985. The genetic material may also be transferred into the plant cell by using polyethylene glycol, Krens, et al., *Nature*, 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high

velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature*, 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta*, 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79, 1859-1863, 1982.

The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl. Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersion*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Hererocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Lolium*, *Zea*, *Triticum*, *Sorghum*, and *Datura*.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension. These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient regeneration will depend on the medium, on the genotype, and on the

history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected. Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

iv. Bacterial Systems

Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (*eg.* structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) [Raibaud *et al.* (1984) *Annu. Rev. Genet.* 18:173]. Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (*lac*) [Chang *et al.* (1977) *Nature* 198:1056], and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (*trp*) [Goeddel *et al.*

(1980) *Nuc. Acids Res.* 8:4057; Yelverton *et al.* (1981) *Nucl. Acids Res.* 9:731; US patent 4,738,921; EP-A-0036776 and EP-A-0121775]. The g-lactamase (*bla*) promoter system [Weissmann (1981) "The cloning of interferon and other mistakes." In *Interferon 3* (ed. I. Gresser)], bacteriophage lambda PL [Shimatake *et al.* (1981) *Nature* 292:128] and T5 [US patent 4,689,406]
5 promoter systems also provide useful promoter sequences.

In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter [US patent 4,551,433]. For example, the *tac* promoter is a hybrid *trp-lac*
10 promoter comprised of both *trp* promoter and *lac* operon sequences that is regulated by the *lac* repressor [Amann *et al.* (1983) *Gene* 25:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci.* 80:21]. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase
15 to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system [Studier *et al.* (1986) *J. Mol. Biol.* 189:113; Tabor *et al.* (1985) *Proc Natl. Acad. Sci.* 82:1074]. In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO-A-0 267 851).

20 In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon [Shine *et al.* (1975) *Nature* 254:34]. The SD sequence is thought to promote binding of mRNA to the ribosome by the
25 pairing of bases between the SD sequence and the 3' end of *E. coli* 16S rRNA [Steitz *et al.* (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological Regulation and Development: Gene Expression* (ed. R.F. Goldberger)]. To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site [Sambrook *et al.* (1989) "Expression of cloned genes in *Escherichia coli*." In *Molecular Cloning: A Laboratory Manual*].

A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide or by either *in vivo* on *in vitro* incubation with a bacterial methionine N-terminal peptidase (EPO-A-0 219 237).

Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria. The resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene [Nagai *et al.* (1984) *Nature* 309:810]. Fusion proteins can also be made with sequences from the *lacZ* [Jia *et al.* (1987) *Gene* 60:197], *trpE* [Allen *et al.* (1987) *J. Biotechnol.* 5:93; Makoff *et al.* (1989) *J. Gen. Microbiol.* 135:11], and *Chey* [EP-A-0 324 647] genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (*eg.* ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated [Miller *et al.* (1989) *Bio/Technology* 7:698].

Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in bacteria [US patent 4,336,336]. The signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro* encoded between the signal peptide fragment and the foreign gene.

DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) [Masui *et al.* (1983), in: *Experimental Manipulation of Gene Expression*; Ghrayeb *et al.* (1984) *EMBO J.* 3:2437] and the *E. coli* alkaline

phosphatase signal sequence (*phoA*) [Oka *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:7212]. As an additional example, the signal sequence of the alpha-amylase gene from various *Bacillus* strains can be used to secrete heterologous proteins from *B. subtilis* [Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EP-A-0 244 042].

- 5 Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in terminating transcription.
- 10 Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

Usually, the above described components, comprising a promoter, signal sequence (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal

15 element (eg. plasmids) capable of stable maintenance in a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy

20 number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to the

25 bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EP-A- 0 127 328). Integrating vectors may also be comprised of bacteriophage or transposon sequences.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline [Davies *et al.* (1978) *Annu. Rev. Microbiol.* 32:469]. Selectable markers may also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable market that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been developed for transformation into many bacteria. For example, expression vectors have been developed for, *inter alia*, the following bacteria: *Bacillus subtilis* [Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EP-A-0 036 259 and EP-A-0 063 953; WO 84/04541], *Escherichia coli* [Shimatake *et al.* (1981) *Nature* 292:128; Amann *et al.* (1985) *Gene* 40:183; Studier *et al.* (1986) *J. Mol. Biol.* 189:113; EP-A-0 036 776, EP-A-0 136 829 and EP-A-0 136 907], *Streptococcus cremoris* [Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655]; *Streptococcus lividans* [Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655], *Streptomyces lividans* [US patent 4,745,056].

Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with CaCl_2 or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by electroporation. Transformation procedures usually vary with the bacterial species to be transformed. See *eg.* [Masson *et al.* (1989) *FEMS Microbiol. Lett.* 60:273; Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EP-A-0 036 259 and EP-A-0 063 953; WO 84/04541, *Bacillus*], [Miller *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:856; Wang *et al.* (1990) *J. Bacteriol.* 172:949, *Campylobacter*], [Cohen *et al.* (1973) *Proc. Natl. Acad. Sci.* 69:2110; Dower *et al.* (1988) *Nucleic Acids Res.* 16:6127; Kushner (1978) "An improved method for transformation of *Escherichia coli* with ColE1-derived plasmids. In *Genetic Engineering: Proceedings of the International Symposium on Genetic Engineering* (eds. H.W. Boyer and S. Nicosia); Mandel *et al.* (1970) *J. Mol. Biol.* 53:159; Taketo (1988) *Biochim. Biophys. Acta* 949:318; *Escherichia*], [Chassy *et al.* (1987) *FEMS Microbiol. Lett.*

44:173 *Lactobacillus*]; [Fiedler *et al.* (1988) *Anal. Biochem* 170:38, *Pseudomonas*]; [Augustin *et al.* (1990) *FEMS Microbiol. Lett.* 66:203, *Staphylococcus*], [Barany *et al.* (1980) *J. Bacteriol.* 144:698; Harlander (1987) "Transformation of *Streptococcus lactis* by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry *et al.* (1981) *Infect. Immun.* 32:1295; Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655; Somkuti *et al.* (1987) *Proc. 4th Evr. Cong. Biotechnology* 1:412, *Streptococcus*].

v. Yeast Expression

Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (eg. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences. Examples include alcohol dehydrogenase (ADH) (EP-A-0 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO-A-0 329 203). The yeast *PHO5* gene, encoding acid phosphatase, also provides useful promoter sequences [Myanohara *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1].

In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (US Patent Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters include promoters which consist of the regulatory sequences of either the *ADH2*, *GAL4*, *GAL10*, OR *PHO5* genes,

combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EP-A-0 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, *inter alia*, [Cohen *et al.* (1980) *Proc. Natl. Acad. Sci. USA* 5 77:1078; Henikoff *et al.* (1981) *Nature* 283:835; Hollenberg *et al.* (1981) *Curr. Topics Microbiol. Immunol.* 96:119; Hollenberg *et al.* (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast *Saccharomyces cerevisiae*," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K.N. Timmis and A. Puhler); Mercerau-Puigalon *et al.* (1980) *Gene* 11:163; Panthier *et al.* (1980) *Curr. Genet.* 2:109;].

- 10 A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.
- 15 Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human superoxide dismutase (SOD) gene, can be
- 20 linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See *eg.* EP-A-0 196 056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (*eg.* ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method,
- 25 therefore, native foreign protein can be isolated (*eg.* WO88/024066).

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The

leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the yeast invertase gene (EP-A-0 012 873; JPO. 62,096,086) and the A-factor gene (US
5 patent 4,588,684). Alternatively, leaders of non-yeast origin, such as an interferon leader, exist that also provide for secretion in yeast (EP-A-0 060 057).

A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino
10 acid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (US Patents 4,546,083 and 4,870,008; EP-A-0 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-factor leaders made with a presequence of a first yeast, but a pro-region from a second yeast alphafactor. (eg. see WO 89/02463.)

15 Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

20 Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (eg. plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast
25 for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEpl24 [Botstein *et al.* (1979) *Gene* 8:17-24], pCl/1 [Brake *et al.* (1984) *Proc. Natl. Acad. Sci USA* 81:4642-4646], and YRp17 [Stinchcomb *et al.* (1982) *J. Mol. Biol.* 158:157]. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and

usually about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20. Enter a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See *eg. Brake et al., supra*.

- 5 Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome [Orr-Weaver *et al.* (1983) *Methods in*
10 *Enzymol.*, 101:228-245]. An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al., supra*. One or more expression construct may integrate, possibly affecting levels of recombinant protein produced [Rine *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:6750]. The chromosomal sequences included in the vector can occur either as a single segment in the vector, which results
15 in the integration of the entire vector, or two segments homologous to adjacent segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may
20 include biosynthetic genes that can be expressed in the yeast host, such as *ADE2*, *HIS4*, *LEU2*, *TRP1*, and *ALG7*, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of *CUP1* allows yeast to grow in the presence of copper ions [Butt *et al.* (1987) *Microbiol.*
25 *Rev.* 51:351].

Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors have been developed for, *inter alia*, the following yeasts: *Candida albicans* [Kurtz, *et al.* (1986) *Mol. Cell. Biol.* 6:142], *Candida maltosa* [Kunze, *et al.* (1985) *J. Basic Microbiol.* 25:141], *Hansenula polymorpha* [Gleeson, *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302], *Kluyveromyces fragilis* [Das, *et al.* (1984) *J. Bacteriol.* 158:1165], *Kluyveromyces lactis* [De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:737; Van den Berg *et al.* (1990) *Bio/Technology* 8:135], *Pichia guilliermondii* [Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141], *Pichia pastoris* [Cregg, *et al.* (1985) *Mol. Cell. Biol.* 5:3376; US Patent Nos. 4,837,148 and 4,929,555], *Saccharomyces cerevisiae* [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163], *Schizosaccharomyces pombe* [Beach and Nurse (1981) *Nature* 300:706], and *Yarrowia lipolytica* [Davidow, *et al.* (1985) *Curr. Genet.* 10:380471 Gaillardin, *et al.* (1985) *Curr. Genet.* 10:49].

Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See eg. [Kurtz *et al.* (1986) *Mol. Cell. Biol.* 6:142; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; *Candida*]; [Gleeson *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302; *Hansenula*]; [Das *et al.* (1984) *J. Bacteriol.* 158:1165; De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:1165; Van den Berg *et al.* (1990) *Bio/Technology* 8:135; *Kluyveromyces*]; [Cregg *et al.* (1985) *Mol. Cell. Biol.* 5:3376; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; US Patent Nos. 4,837,148 and 4,929,555; *Pichia*]; [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163 *Saccharomyces*]; [Beach and Nurse (1981) *Nature* 300:706; *Schizosaccharomyces*]; [Davidow *et al.* (1985) *Curr. Genet.* 10:39; Gaillardin *et al.* (1985) *Curr. Genet.* 10:49; *Yarrowia*].

Antibodies

As used herein, the term “antibody” refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An “antibody combining site” is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. “Antibody”

includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanised antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

Antibodies against the proteins of the invention are useful for affinity chromatography, immunoassays, and distinguishing/identifying Neisserial proteins.

- 5 Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 μ g/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by *in vitro* immunization using methods known in the art, which for the purposes of this invention is considered equivalent to *in vivo* immunization. Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25°C for one hour, followed by incubating at 4°C for 2-18 hours. The serum is recovered by centrifugation (*eg.* 1,000g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.
- 20 Monoclonal antibodies are prepared using the standard method of Kohler & Milstein [*Nature* (1975) 256:495-96], or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells expressing membrane-bound immunoglobulin specific for the antigen bind to the plate, and are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (*eg.* hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for the production of antibodies which bind specifically to the immunizing antigen
- 25
- 30

(and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either *in vitro* (eg. in tissue culture bottles or hollow fiber reactors), or *in vivo* (as ascites in mice).

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly ^{32}P and ^{125}I), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3',5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example, ^{125}I may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with ^{125}I , or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

Pharmaceutical Compositions

Pharmaceutical compositions can comprise either polypeptides, antibodies, or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of

therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgement of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

Delivery Methods

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal or transcutaneous applications (eg. see WO98/20734), needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Vaccines

Vaccines according to the invention may either be prophylactic (*ie.* to prevent infection) or therapeutic (*ie.* to treat disease after infection).

Such vaccines comprise immunising antigen(s), immunogen(s), polypeptide(s), protein(s) or nucleic acid, usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the antigen or immunogen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, etc. pathogens.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59™ (WO 90/14837; Chapter 10 in *Vaccine design: the subunit and adjuvant approach*, eds. Powell & Newman, Plenum Press 1995), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalene, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) Ribi™ adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial

cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (Detox™); (3) saponin adjuvants, such as Stimulon™ (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (*eg.* IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, *etc.*), interferons (*eg.* gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), *etc.*; and (6) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59™ are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), *etc.*

The immunogenic compositions (*eg.* the immunising antigen/immunogen/polypeptide/protein/nucleic acid, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, *etc.* Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles.

Typically, the immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

Immunogenic compositions used as vaccines comprise an immunologically effective amount of the antigenic or immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (*eg.* nonhuman primate, primate, *etc.*), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation,

and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

The immunogenic compositions are conventionally administered parenterally, *eg.* by injection, either subcutaneously, intramuscularly, or transdermally/transcutaneously (*eg.* WO98/20734).

5 Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

10 As an alternative to protein-based vaccines, DNA vaccination may be employed [*eg.* Robinson & Torres (1997) *Seminars in Immunology* 9:271-283; Donnelly *et al.* (1997) *Annu Rev Immunol* 15:617-648; see later herein].

Gene Delivery Vehicles

15 Gene therapy vehicles for delivery of constructs including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in *in vivo* or *ex vivo* modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence *in vivo* can be either constitutive or regulated.

20 The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 25 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

Retroviral vectors are well known in the art and we contemplate that any retroviral gene therapy vector is employable in the invention, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retroviruses

eg. MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site
5 from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see US patent 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA
10 by incorporation of a chimeric integrase enzyme into the retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant
15 vector particles. Preferably, the packaging cell lines are made from human parent cells (eg. HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia, Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly
20 preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC No. VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Maryland or
25 isolated from known sources using commonly available techniques.

Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698,

WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, US 5,219,740, US 4,405,712, US 4,861,719, US 4,980,289, US 4,777,127, US 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671, WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102, WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654.

Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (*ie.* there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in US Patent 5,478,745. Still other vectors are those disclosed in Carter US Patent 4,797,368 and

Muzyczka US Patent 5,139,941, Chartejee US Patent 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in US 5,354,678, US 5,173,414, US 5,139,941, and US 5,252,479.

The gene therapy vectors of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in US 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar Institute), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 and WO92/07945, HSV Us3::pgC-lacZ described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with the ATCC as accession numbers ATCC VR-977 and ATCC VR-260.

Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in US patents 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in US Serial No. 08/405,627, filed March 15, 1995, WO94/21792, WO92/10578, WO95/07994, US 5,091,309 and US 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Maryland or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see USSN 08/679640).

DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems. Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

Other viral vectors suitable for use in the present invention include those derived from poliovirus, for example ATCC VR-58 and those described in Evans, *Nature* 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem* L401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in US 4,603,112 and US 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in US 5,166,057 and in Enami (1990) *Proc Natl Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus, for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Trinita virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

Delivery of the compositions of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see US Serial No. 08/366,787, filed December 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see US Serial No.08/240,030, filed May 9,

1994, and US Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in US Patent 5,149,655, ionizing radiation as described in US5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and
5 in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

Particle mediated gene transfer may be employed, for example see US Serial No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting
10 ligands such as asialoorosomucoid, as described in Wu & Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

Naked DNA may also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and US 5,580,859. Uptake efficiency may be improved using biodegradable latex
15 beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

Liposomes that can act as gene delivery vehicles are described in US 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in USSN. 60/023,867, on non-viral
20 delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate
25 DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al* (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods
30 for gene delivery that can be used for delivery of the coding sequence include, for example, use of

hand-held gene transfer particle gun, as described in US 5,149,655; use of ionizing radiation for activating transferred gene, as described in US 5,206,152 and WO92/11033

Exemplary liposome and polycationic gene delivery vehicles are those described in US 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697; and WO91/14445; in EP-0524968; and in Stryer, 5 *Biochemistry*, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will 10 be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

Delivery Methods

Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) *in vitro* for expression 15 of recombinant proteins. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of 20 administration include oral and pulmonary administration, suppositories, and transdermal or transcutaneous applications (*eg.* see WO98/20734), needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in *eg.* WO93/14778. Examples of cells useful in *ex vivo* applications 25 include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Polynucleotide and polypeptide pharmaceutical compositions

In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

A. Polypeptides

- One example are polypeptides which include, without limitation: asialoglycoprotein (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of plasmodium falciparum known as RII.

B. Hormones, Vitamins, etc.

Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.

C. Polyalkylenes, Polysaccharides, etc.

Also, polyalkylene glycol can be included with the desired polynucleotides/polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethylene glycol. In addition, mono-, di-, or polysaccharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

D. Lipids, and Liposomes

The desired polynucleotide/polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim.*

5 *Biophys. Acta.* 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified
10 transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See, also, Felgner *supra*). Other commercially available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boehringer). Other cationic liposomes can be
15 prepared from readily available materials using techniques well known in the art. See, *eg.* Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include
20 phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs),
25 or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See *eg.* Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) *Cell* 17:77; Deamer & Bangham (1976) *Biochim. Biophys. Acta* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA*

76:3348); Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

E. Lipoproteins

- 5 In addition, lipoproteins can be included with the polynucleotide/polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with
10 the polynucleotide to be delivered, no other targeting ligand is included in the composition.

Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

- 15 A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C, and E, over time these lipoproteins lose A and acquire C and E apoproteins. VLDL comprises A, B, C, and E apoproteins, LDL comprises apoprotein B; and HDL comprises apoproteins A, C, and E.

- The amino acid of these apoproteins are known and are described in, for example, Breslow (1985)
20 *Annu Rev. Biochem* 54:699; Law (1986) *Adv. Exp Med. Biol.* 151:162; Chen (1986) *J Biol Chem* 261:12918; Kane (1980) *Proc Natl Acad Sci USA* 77:2465; and Utermann (1984) *Hum Genet* 65:232.

- Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid
25 content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol. (supra)*; Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J Clin. Invest* 64:743-750. Lipoproteins can also be produced by *in vitro* or recombinant methods by expression of the apoprotein genes in a desired host cell. See, for example, 5 Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acta* 30: 443. Lipoproteins can also be purchased from commercial suppliers, such as Biomedical Technologies, Inc., Stoughton, Massachusetts, USA. Further description of lipoproteins can be found in Zuckermann *et al.* PCT/US97/14465.

F. Polycationic Agents

- 10 Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide/polypeptide to be delivered.

Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both *in vitro*, *ex vivo*, and *in vivo* applications. Polycationic agents can 15 be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, etc.

The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine, and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, coat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful 20 as nucleic acid condensing agents. Briefly, transcriptional factors such as C/CEBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

Organic polycationic agents include: spermine, spermidine, and putrescine.

The dimensions and of the physical properties of a polycationic agent can be extrapolated from the 25 list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin™, and lipofectAMINE™ are monomers that form polycationic complexes when combined with polynucleotides/polypeptides.

Immunodiagnostic Assays

5 Neisserial antigens of the invention can be used in immunoassays to detect antibody levels (or, conversely, anti-Neisserial antibodies can be used to detect antigen levels). Immunoassays based on well defined, recombinant antigens can be developed to replace invasive diagnostics methods. Antibodies to Neisserial proteins within biological samples, including for example, blood or serum samples, can be detected. Design of the immunoassays is subject to a great deal of variation, and
10 a variety of these are known in the art. Protocols for the immunoassay may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the probe are also known; examples of which
15 are assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the compositions of the invention, in suitable containers, along with the remaining reagents and materials (for example, suitable buffers, salt
20 solutions, *etc.*) required for the conduct of the assay, as well as suitable set of assay instructions.

Nucleic Acid Hybridisation

“Hybridization” refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions that favor
25 hydrogen bonding. Factors that affect this bonding include: the type and volume of solvent; reaction temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequences; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook *et al.*
30 [*supra*] Volume 2, chapter 9, pages 9.47 to 9.57.

"Stringency" refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200°C below the calculated T_m of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See Sambrook *et al.* at page 9.50.

Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1 µg for a plasmid or phage digest to 10^{-9} to 10^{-8} g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting, hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes can be used. For example, a single-copy yeast gene can be detected with an exposure time of only 1 hour starting with 1 µg of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of 10^8 cpm/µg. For a single-copy mammalian gene a conservative approach would start with 10 µg of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than 10^8 cpm/µg, resulting in an exposure time of ~24 hours.

Several factors can affect the melting temperature (T_m) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$T_m = 81 + 16.6(\log_{10} C_i) + 0.4[\%(G + C)] - 0.6(\%\text{formamide}) - 600/n - 1.5(\%\text{mismatch}).$$

where C_i is the salt concentration (monovalent ions) and n is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (*ie.* stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

In general, convenient hybridization temperatures in the presence of 50% formamide are 42°C for a probe with is 95% to 100% homologous to the target fragment, 37°C for 90% to 95% homology, and 32°C for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be washed at high stringency and reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

20 Nucleic Acid Probe Assays

Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

25 The nucleic acid probes will hybridize to the Neisserial nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native Neisserial sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

The probe sequence need not be identical to the Neisserial sequence (or its complement) — some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Neisserial sequence may
5 also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Neisserial sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Neisserial sequence in order to hybridize therewith and
10 thereby form a duplex which can be detected.

The exact length and sequence of the probe will depend on the hybridization conditions, such as temperature, salt condition and the like. For example, for diagnostic applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably at least 30 nucleotides, although it may be
15 shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

Probes may be produced by synthetic procedures, such as the triester method of Matteucci *et al.* [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea *et al.* [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

20 The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated *eg.* backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase *in vivo* half-life, alter RNA affinity, increase nuclease resistance *etc.* [*eg.* see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as
25 peptide nucleic acids may also be used [*eg.* see Corey (1997) *TIBTECH* 15:224-229; Buchardt *et al.* (1993) *TIBTECH* 11:384-386].

Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acids. The assay is described in: Mullis *et al.* [*Meth. Enzymol.* (1987) 155: 335-350]; US patents 4,683,195 and 4,683,202. Two “primer” nucleotides hybridize

with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Neisserial sequence.

- 5 A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Neisserial sequence (or its complement).
- 10 Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al* [*supra*]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes containing the labeled probe are detected.
- 15 Typically, the probe is labelled with a radioactive moiety.

BRIEF DESCRIPTION OF THE DRAWINGS

- Figures 1-7** show biochemical data and sequence analysis pertaining to Examples 1, 2, 3, 7, 13, 16 and 19, respectively, with ORFs 40, 38, 44, 52, 114, 41 and 124.. M1 and M2 are molecular weight markers. Arrows indicate the position of the main recombinant product or, in Western blots, the position of the main *N.meningitidis* immunoreactive band. TP indicates *N.meningitidis* total protein extract; OMV indicates *N.meningitidis* outer membrane vesicle preparation. In bactericidal assay results: a diamond (◆) shows preimmune data; a triangle (▲) shows GST control data; a circle (●) shows data with recombinant *N.meningitidis* protein. Computer analyses show a hydrophilicity plot (upper), an antigenic index plot (middle), and an AMPHI analysis (lower). The
- 20 AMPHI program has been used to predict T-cell epitopes [Gao *et al.* (1989) *J. Immunol.* 143:3007; Roberts *et al.* (1996) *AIDS Res Hum Retrovir* 12:593; Quakyi *et al.* (1992) *Scand J Immunol* suppl.11:9) and is available in the Protean package of DNASTAR, Inc. (1228 South Park Street, Madison, Wisconsin 53715 USA).
- 25

EXAMPLES

The examples describe nucleic acid sequences which have been identified in *N.meningitidis*, along with their putative translation products. Not all of the nucleic acid sequences are complete *ie.* they encode less than the full-length wild-type protein. It is believed at present that none of the DNA sequences described herein have significant homologs in *N.gonorrhoeae*.

The examples are generally in the following format:

- a nucleotide sequence which has been identified in *N.meningitidis* (strain B)
- the putative translation product of this sequence
- a computer analysis of the translation product based on database comparisons
- a corresponding gene and protein sequence identified in *N.meningitidis* (strain A)
- a description of the characteristics of the proteins which indicates that they might be suitably antigenic
- results of biochemical analysis (expression, purification, ELISA, FACS *etc.*)

The examples typically include details of sequence homology between species and strains. Proteins that are similar in sequence are generally similar in both structure and function, and the homology often indicates a common evolutionary origin. Comparison with sequences of proteins of known function is widely used as a guide for the assignment of putative protein function to a new sequence and has proved particularly useful in whole-genome analyses.

Sequence comparisons were performed at NCBI (<http://www.ncbi.nlm.nih.gov>) using the algorithms BLAST, BLAST2, BLASTn, BLASTp, tBLASTn, BLASTx, & tBLASTx [*eg.* see also Altschul *et al.* (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* 25:2289-3402]. Searches were performed against the following databases: non-redundant GenBank+EMBL+DDBJ+PDB sequences and non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR sequences.

Dots within nucleotide sequences (*eg.* position 288 in Example 12) represent nucleotides which have been arbitrarily introduced in order to maintain a reading frame. In the same way, double-underlined nucleotides were removed. Lower case letters (*eg.* position 589 in Example 12) represent ambiguities which arose during alignment of independent sequencing reactions (some of

the nucleotide sequences in the examples are derived from combining the results of two or more experiments).

Nucleotide sequences were scanned in all six reading frames to predict the presence of hydrophobic domains using an algorithm based on the statistical studies of Esposti *et al.* [Critical evaluation of the hydropathy of membrane proteins (1990) *Eur J Biochem* 190:207-219]. These domains represent potential transmembrane regions or hydrophobic leader sequences.

Open reading frames were predicted from fragmented nucleotide sequences using the program ORFFINDER (NCBI).

Underlined amino acid sequences indicate possible transmembrane domains or leader sequences in the ORFs, as predicted by the PSORT algorithm (<http://www.psort.nibb.ac.jp>). Functional domains were also predicted using the MOTIFS program (GCG Wisconsin & PROSITE).

Various tests can be used to assess the *in vivo* immunogenicity of the proteins identified in the examples. For example, the proteins can be expressed recombinantly and used to screen patient sera by immunoblot. A positive reaction between the protein and patient serum indicates that the patient has previously mounted an immune response to the protein in question *ie.* the protein is an immunogen. This method can also be used to identify immunodominant proteins.

The recombinant protein can also be conveniently used to prepare antibodies *eg.* in a mouse. These can be used for direct confirmation that a protein is located on the cell-surface. Labelled antibody (*eg.* fluorescent labelling for FACS) can be incubated with intact bacteria and the presence of label on the bacterial surface confirms the location of the protein.

In particular, the following methods (A) to (S) were used to express, purify and biochemically characterise the proteins of the invention:

A) Chromosomal DNA preparation

N.meningitidis strain 2996 was grown to exponential phase in 100ml of GC medium, harvested by centrifugation, and resuspended in 5ml buffer (20% Sucrose, 50mM Tris-HCl, 50mM EDTA, pH8). After 10 minutes incubation on ice, the bacteria were lysed by adding 10ml lysis solution (50mM NaCl, 1% Na-Sarkosyl, 50µg/ml Proteinase K), and the suspension was incubated at 37°C for 2

hours. Two phenol extractions (equilibrated to pH 8) and one ChCl_3 /isoamylalcohol (24:1) extraction were performed. DNA was precipitated by addition of 0.3M sodium acetate and 2 volumes ethanol, and was collected by centrifugation. The pellet was washed once with 70% ethanol and redissolved in 4ml buffer (10mM Tris-HCl, 1mM EDTA, pH 8). The DNA
5 concentration was measured by reading the OD at 260 nm.

B) Oligonucleotide design

Synthetic oligonucleotide primers were designed on the basis of the coding sequence of each ORF, using (a) the meningococcus B sequence when available, or (b) the gonococcus/meningococcus A sequence, adapted to the codon preference usage of meningococcus as necessary. Any predicted
10 signal peptides were omitted, by deducing the 5'-end amplification primer sequence immediately downstream from the predicted leader sequence.

The 5' primers included two restriction enzyme recognition sites (*Bam*HI-*Nde*I, *Bam*HI-*Nhe*I, or *Eco*RI-*Nhe*I, depending on the gene's own restriction pattern); the 3' primers included a *Xho*I restriction site. This procedure was established in order to direct the cloning of each amplification
15 product (corresponding to each ORF) into two different expression systems: pGEX-KG (using either *Bam*HI-*Xho*I or *Eco*RI-*Xho*I), and pET21b+ (using either *Nde*I-*Xho*I or *Nhe*I-*Xho*I).

5'-end primer tail: CGCGGATCCCATATG (*Bam*HI-*Nde*I)

CGCGGATCCGCTAGC (*Bam*HI-*Nhe*I)

CCGGAATTCTAGCTAGC (*Eco*RI-*Nhe*I)

20 3'-end primer tail: CCCGCTCGAG (*Xho*I)

As well as containing the restriction enzyme recognition sequences, the primers included nucleotides which hybridised to the sequence to be amplified. The number of hybridizing nucleotides depended on the melting temperature of the whole primer, and was determined for each primer using the formulae:

25 $T_m = 4 (G+C) + 2 (A+T)$ (tail excluded)

$T_m = 64.9 + 0.41 (\% \text{ GC}) - 600/N$ (whole primer)

The average melting temperature of the selected oligos were 65-70°C for the whole oligo and 50-55°C for the hybridising region alone.

Table I shows the forward and reverse primers used for each amplification. Oligos were synthesized by a Perkin Elmer 394 DNA/RNA Synthesizer, eluted from the columns in 2ml NH_4OH , and deprotected by 5 hours incubation at 56°C . The oligos were precipitated by addition of 0.3M Na-Acetate and 2 volumes ethanol. The samples were then centrifuged and the pellets resuspended in either 100 μl or 1ml of water. OD_{260} was determined using a Perkin Elmer Lambda Bio spectrophotometer and the concentration was determined and adjusted to 2-10pmol/ μl .

C) Amplification

The standard PCR protocol was as follows: 50-200ng of genomic DNA were used as a template in the presence of 20-40 μM of each oligo, 400-800 μM dNTPs solution, 1x PCR buffer (including 1.5mM MgCl_2), 2.5 units *TaqI* DNA polymerase (using Perkin-Elmer AmpliTaq, GIBCO Platinum, Pwo DNA polymerase, or Tahara Shuzo Taq polymerase).

In some cases, PCR was optimised by the addition of 10 μl DMSO or 50 μl 2M betaine.

After a hot start (adding the polymerase during a preliminary 3 minute incubation of the whole mix at 95°C), each sample underwent a double-step amplification: the first 5 cycles were performed using as the hybridization temperature the one of the oligos excluding the restriction enzymes tail, followed by 30 cycles performed according to the hybridization temperature of the whole length oligos. The cycles were followed by a final 10 minute extension step at 72°C .

The standard cycles were as follows:

	Denaturation	Hybridisation	Elongation
First 5 cycles	30 seconds 95°C	30 seconds $50-55^\circ\text{C}$	30-60 seconds 72°C
Last 30 cycles	30 seconds 95°C	30 seconds $65-70^\circ\text{C}$	30-60 seconds 72°C

The elongation time varied according to the length of the ORF to be amplified.

The amplifications were performed using either a 9600 or a 2400 Perkin Elmer GeneAmp PCR System. To check the results, 1/10 of the amplification volume was loaded onto a 1-1.5% agarose gel and the size of each amplified fragment compared with a DNA molecular weight marker.

5 The amplified DNA was either loaded directly on a 1% agarose gel or first precipitated with ethanol and resuspended in a suitable volume to be loaded on a 1% agarose gel. The DNA fragment corresponding to the right size band was then eluted and purified from gel, using the Qiagen Gel Extraction Kit, following the instructions of the manufacturer. The final volume of the DNA fragment was 30µl or 50µl of either water or 10mM Tris, pH 8.5.

D) Digestion of PCR fragments

10 The purified DNA corresponding to the amplified fragment was split into 2 aliquots and double-digested with:

- *NdeI/XhoI* or *NheI/XhoI* for cloning into pET-21b+ and further expression of the protein as a C-terminus His-tag fusion
- *BamHI/XhoI* or *EcoRI/XhoI* for cloning into pGEX-KG and further expression of the
15 protein as N-terminus GST fusion.
- *EcoRI/PstI*, *EcoRI/SalI*, *SalI/PstI* for cloning into pGex-His and further expression of the protein as N-terminus His-tag fusion

20 Each purified DNA fragment was incubated (37°C for 3 hours to overnight) with 20 units of each restriction enzyme (New England Biolabs) in a either 30 or 40µl final volume in the presence of the appropriate buffer. The digestion product was then purified using the QIAquick PCR purification kit, following the manufacturer's instructions, and eluted in a final volume of 30 or 50µl of either water or 10mM Tris-HCl, pH 8.5. The final DNA concentration was determined by 1% agarose gel electrophoresis in the presence of titrated molecular weight marker.

E) Digestion of the cloning vectors (pET22B, pGEX-KG, pTRC-His A, and pGex-His)

25 10µg plasmid was double-digested with 50 units of each restriction enzyme in 200µl reaction volume in the presence of appropriate buffer by overnight incubation at 37°C. After loading the

whole digestion on a 1% agarose gel, the band corresponding to the digested vector was purified from the gel using the Qiagen QIAquick Gel Extraction Kit and the DNA was eluted in 50µl of 10mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD₂₆₀ of the sample, and adjusted to 50µg/µl. 1µl of plasmid was used for each cloning procedure.

- 5 The vector pGEX-His is a modified pGEX-2T vector carrying a region encoding six histidine residues upstream to the thrombin cleavage site and containing the multiple cloning site of the vector pTRC99 (Pharmacia).

F) Cloning

- 10 The fragments corresponding to each ORF, previously digested and purified, were ligated in both pET22b and pGEX-KG. In a final volume of 20µl, a molar ratio of 3:1 fragment/vector was ligated using 0.5µl of NEB T4 DNA ligase (400 units/µl), in the presence of the buffer supplied by the manufacturer. The reaction was incubated at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit", following the manufacturer's instructions.

- 15 In order to introduce the recombinant plasmid in a suitable strain, 100µl *E. coli* DH5 competent cells were incubated with the ligase reaction solution for 40 minutes on ice, then at 37°C for 3 minutes, then, after adding 800µl LB broth, again at 37°C for 20 minutes. The cells were then centrifuged at maximum speed in an Eppendorf microfuge and resuspended in approximately 200µl of the supernatant. The suspension was then plated on LB ampicillin (100mg/ml).

- 20 The screening of the recombinant clones was performed by growing 5 randomly-chosen colonies overnight at 37°C in either 2ml (pGEX or pTC clones) or 5ml (pET clones) LB broth + 100µg/ml ampicillin. The cells were then pelleted and the DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions, to a final volume of 30µl. 5µl of each individual miniprep (approximately 1g) were digested with either *NdeI/XhoI* or *BamHI/XhoI* and the whole digestion loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1Kb DNA Ladder, GIBCO). The screening of the positive clones was made on the base of the correct insert size.
- 25

G) Expression

Each ORF cloned into the expression vector was transformed into the strain suitable for expression of the recombinant protein product. 1µl of each construct was used to transform 30µl of *E.coli* BL21 (pGEX vector), *E.coli* TOP 10 (pTRC vector) or *E.coli* BL21-DE3 (pET vector), as described
5 above. In the case of the pGEX-His vector, the same *E.coli* strain (W3110) was used for initial cloning and expression. Single recombinant colonies were inoculated into 2ml LB+Amp (100µg/ml), incubated at 37°C overnight, then diluted 1:30 in 20ml of LB+Amp (100µg/ml) in 100ml flasks, making sure that the OD₆₀₀ ranged between 0.1 and 0.15. The flasks were incubated at 30°C into gyratory water bath shakers until OD indicated exponential growth suitable for
10 induction of expression (0.4-0.8 OD for pET and pTRC vectors; 0.8-1 OD for pGEX and pGEX-His vectors). For the pET, pTRC and pGEX-His vectors, the protein expression was induced by addition of 1mM IPTG, whereas in the case of pGEX system the final concentration of IPTG was 0.2mM. After 3 hours incubation at 30°C, the final concentration of the sample was checked by OD. In order to check expression, 1ml of each sample was removed, centrifuged in a microfuge,
15 the pellet resuspended in PBS, and analysed by 12% SDS-PAGE with Coomassie Blue staining. The whole sample was centrifuged at 6000g and the pellet resuspended in PBS for further use.

H) GST-fusion proteins large-scale purification.

A single colony was grown overnight at 37°C on LB+Amp agar plate. The bacteria were inoculated into 20ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were
20 diluted 1:30 into 600ml of fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.8-1. Protein expression was induced with 0.2mM IPTG followed by three hours incubation. The culture was centrifuged at 8000rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5ml cold PBS. The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed twice and centrifuged again.
25 The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia) (previously washed with PBS) and incubated at room temperature for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10ml cold PBS for 10 minutes, resuspended in 1ml cold PBS, and loaded on a disposable column. The resin was washed twice with 2ml cold PBS until the flow-through reached OD₂₈₀ of 0.02-0.06. The GST-fusion
30 protein was eluted by addition of 700µl cold Glutathione elution buffer (10mM reduced

glutathione, 50mM Tris-HCl) and fractions collected until the OD_{280} was 0.1. 21 μ l of each fraction were loaded on a 12% SDS gel using either Biorad SDS-PAGE Molecular weight standard broad range (M1) (200, 116.25, 97.4, 66.2, 45, 31, 21.5, 14.4, 6.5 kDa) or Amersham Rainbow Marker (M2) (220, 66, 46, 30, 21.5, 14.3 kDa) as standards. As the MW of GST is 26kDa, this value must be added to the MW of each GST-fusion protein.

I) His-fusion solubility analysis

To analyse the solubility of the His-fusion expression products, pellets of 3ml cultures were resuspended in buffer M1 [500 μ l PBS pH 7.2]. 25 μ l lysozyme (10mg/ml) was added and the bacteria were incubated for 15 min at 4°C. The pellets were sonicated for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed twice and then separated again into pellet and supernatant by a centrifugation step. The supernatant was collected and the pellet was resuspended in buffer M2 [8M urea, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] and incubated for 3 to 4 hours at 4°C. After centrifugation, the supernatant was collected and the pellet was resuspended in buffer M3 [6M guanidinium-HCl, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] overnight at 4°C. The supernatants from all steps were analysed by SDS-PAGE.

J) His-fusion large-scale purification.

A single colony was grown overnight at 37°C on a LB + Amp agar plate. The bacteria were inoculated into 20ml of LB+Amp liquid culture and incubated overnight in a water bath shaker. Bacteria were diluted 1:30 into 600ml fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD_{550} 0.6-0.8. Protein expression was induced by addition of 1mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000rpm at 4°C, the supernatant was discarded and the bacterial pellet was resuspended in 7.5ml of either (i) cold buffer A (300mM NaCl, 50mM phosphate buffer, 10mM imidazole, pH 8) for soluble proteins or (ii) buffer B (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8) for insoluble proteins.

The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again.

For insoluble proteins, the supernatant was stored at -20°C, while the pellets were resuspended in 2ml buffer C (6M guanidine hydrochloride, 100mM phosphate buffer, 10mM Tris-HCl, pH 7.5) and treated in a homogenizer for 10 cycles. The product was centrifuged at 13000rpm for 40 minutes.

Supernatants were collected and mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with either buffer A or buffer B, as appropriate) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10ml buffer A or B for 10 minutes, resuspended in 1ml buffer A or B and loaded on a disposable column. The resin was washed at either (i) 4°C with 2ml cold buffer A or (ii) room temperature with 2ml buffer B, until the flow-through reached OD₂₈₀ of 0.02-0.06.

- 10 The resin was washed with either (i) 2ml cold 20mM imidazole buffer (300mM NaCl, 50mM phosphate buffer, 20mM imidazole, pH 8) or (ii) buffer D (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl of either (i) cold elution buffer A (300mM NaCl, 50mM phosphate buffer, 250mM imidazole, pH 8) or (ii) elution buffer B (urea 8M, 10mM Tris-HCl, 15 100mM phosphate buffer, pH 4.5) and fractions collected until the O.D₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

K) His-fusion proteins renaturation

- 10% glycerol was added to the denatured proteins. The proteins were then diluted to 20µg/ml using dialysis buffer I (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 20 0.5mM oxidised glutathione, 2M urea, pH 8.8) and dialysed against the same buffer at 4°C for 12-14 hours. The protein was further dialysed against dialysis buffer II (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C. Protein concentration was evaluated using the formula:

$$\text{Protein (mg/ml)} = (1.55 \times \text{OD}_{280}) - (0.76 \times \text{OD}_{260})$$

25 L) His-fusion large-scale purification

500ml of bacterial cultures were induced and the fusion proteins were obtained soluble in buffer M1, M2 or M3 using the procedure described above. The crude extract of the bacteria was loaded

onto a Ni-NTA superflow column (Qiagen) equilibrated with buffer M1, M2 or M3 depending on the solubilization buffer of the fusion proteins. Unbound material was eluted by washing the column with the same buffer. The specific protein was eluted with the corresponding buffer containing 500mM imidazole and dialysed against the corresponding buffer without imidazole.

- 5 After each run the columns were sanitized by washing with at least two column volumes of 0.5 M sodium hydroxide and reequilibrated before the next use.

M) Mice immunisations

- 20µg of each purified protein were used to immunise mice intraperitoneally. In the case of ORF 44, CD1 mice were immunised with Al(OH)₃ as adjuvant on days 1, 21 and 42, and immune response
10 was monitored in samples taken on day 56. For ORF 40, CD1 mice were immunised using Freund's adjuvant, rather than Al(OH)₃, and the same immunisation protocol was used, except that the immune response was measured on day 42, rather than 56. Similarly, for ORF 38, CD1 mice were immunised with Freund's adjuvant, but the immune response was measured on day 49.

N) ELISA assay (sera analysis)

- 15 The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 7ml of Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10000rpm. The
20 supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated for 2 hours at room temperature and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in
25 water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 90 minutes at 37°C. Wells were washed three times with PBT. 100µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at

37°C. Wells were washed three times with PBT buffer. 100µl of substrate buffer for HRP (25ml of citrate buffer pH5, 10mg of O-phenildiamine and 10µl of H₂O) were added to each well and the plates were left at room temperature for 20 minutes. 100µl H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA was considered positive when OD₄₉₀ was 2.5 times the respective pre-immune sera.

O) FACSscan bacteria Binding Assay procedure.

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 4 tubes containing 8ml each Mueller-Hinton Broth (Difco) containing 0.25% glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.35-0.5. The culture was centrifuged for 10 minutes at 4000rpm. The supernatant was discarded and the pellet was resuspended in blocking buffer (1% BSA, 0.4% NaN₃) and centrifuged for 5 minutes at 4000rpm. Cells were resuspended in blocking buffer to reach OD₆₂₀ of 0.07. 100µl bacterial cells were added to each well of a Costar 96 well plate. 100µl of diluted (1:200) sera (in blocking buffer) were added to each well and plates incubated for 2 hours at 4°C. Cells were centrifuged for 5 minutes at 4000rpm, the supernatant aspirated and cells washed by addition of 200µl/well of blocking buffer in each well. 100µl of R-Phicoerytrin conjugated F(ab)₂ goat anti-mouse, diluted 1:100, was added to each well and plates incubated for 1 hour at 4°C. Cells were spun down by centrifugation at 4000rpm for 5 minutes and washed by addition of 200µl/well of blocking buffer. The supernatant was aspirated and cells resuspended in 200µl/well of PBS, 0.25% formaldehyde. Samples were transferred to FACSscan tubes and read. The condition for FACSscan setting were: FL1 on, FL2 and FL3 off; FSC-H threshold:92; FSC PMT Voltage: E 02; SSC PMT: 474; Amp. Gains 7.1; FL-2 PMT: 539; compensation values: 0.

P) OMV preparations

Bacteria were grown overnight on 5 GC plates, harvested with a loop and resuspended in 10 ml 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30 minutes and the bacteria disrupted by sonication for 10 minutes on ice (50% duty cycle, 50% output). Unbroken cells were removed by centrifugation at 5000g for 10 minutes and the total cell envelope fraction recovered by centrifugation

at 50000g at 4°C for 75 minutes. To extract cytoplasmic membrane proteins from the crude outer membranes, the whole fraction was resuspended in 2% sarkosyl (Sigma) and incubated at room temperature for 20 minutes. The suspension was centrifuged at 10000g for 10 minutes to remove aggregates, and the supernatant further ultracentrifuged at 50000g for 75 minutes to pellet the outer membranes. The outer membranes were resuspended in 10mM Tris-HCl, pH8 and the protein concentration measured by the Bio-Rad Protein assay, using BSA as a standard.

Q) Whole Extracts preparation

Bacteria were grown overnight on a GC plate, harvested with a loop and resuspended in 1ml of 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30 minutes.

10 R) Western blotting

Purified proteins (500ng/lane), outer membrane vesicles (5µg) and total cell extracts (25µg) derived from MenB strain 2996 were loaded on 15% SDS-PAGE and transferred to a nitrocellulose membrane. The transfer was performed for 2 hours at 150mA at 4°C, in transferring buffer (0.3 % Tris base, 1.44 % glycine, 20% methanol). The membrane was saturated by overnight incubation at 4°C in saturation buffer (10% skimmed milk, 0.1% Triton X100 in PBS). The membrane was washed twice with washing buffer (3% skimmed milk, 0.1% Triton X100 in PBS) and incubated for 2 hours at 37°C with mice sera diluted 1:200 in washing buffer. The membrane was washed twice and incubated for 90 minutes with a 1:2000 dilution of horseradish peroxidase labelled anti-mouse Ig. The membrane was washed twice with 0.1% Triton X100 in PBS and developed with the Opti-4CN Substrate Kit (Bio-Rad). The reaction was stopped by adding water.

S) Bactericidal assay

MC58 strain was grown overnight at 37°C on chocolate agar plates. 5-7 colonies were collected and used to inoculate 7ml Mueller-Hinton broth. The suspension was incubated at 37°C on a nutator and let to grow until OD₆₂₀ was 0.5-0.8. The culture was aliquoted into sterile 1.5ml Eppendorf tubes and centrifuged for 20 minutes at maximum speed in a microfuge. The pellet was washed once in Gey's buffer (Gibco) and resuspended in the same buffer to an OD₆₂₀ of 0.5, diluted 1:20000 in Gey's buffer and stored at 25°C.

50µl of Gey's buffer/1% BSA was added to each well of a 96-well tissue culture plate. 25µl of diluted mice sera (1:100 in Gey's buffer/0.2% BSA) were added to each well and the plate incubated at 4°C. 25µl of the previously described bacterial suspension were added to each well. 25µl of either heat-inactivated (56°C waterbath for 30 minutes) or normal baby rabbit complement were added to each well. Immediately after the addition of the baby rabbit complement, 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 0). The 96-well plate was incubated for 1 hour at 37°C with rotation and then 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 1). After overnight incubation the colonies corresponding to time 0 and time 1 hour were counted.

Table II gives a summary of the cloning, expression and purification results.

Example 1

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1>:

```

1  ..ACACTGTTGT TTGCAACGGT TCAGGCAAGT GCTAACCAAT GAAGAGCAAG
51  AAGAAGATTT ATATTTAGAC CCCGTACAAC GCACTGTTGC CGTGTGATA
101 GTCAATTCCG ATAAAGAAGG CACGGGAGAA AAAGAAAAAG TAGAAGAAAA
151 TTCAGATTGG GCAGTATATT TCAACGAGAA AGGAGTACTA ACAGCCAGAG
201 AAATCACCyT CAAAGCCGGC GACAACCTGA AAATCAAACA AACGGGCACA
251 AACTTCACCT ACTCGCTGAA AAAAGACCTC AcAGATCTGA CCAGTGTGG
301 AACTGAAAAA TTATCGTTTA GCGCAAACGG CAATAAAGTC AACATcACAA
351 GCGACACCAA AGGCTTGAAT TTTGCGAAAG AAACGGCTGG sACGAACGgC
401 GACACCACGG TTCATCTGAA CGGTATTGGT TCGACTTTGA CCGATACGCT
451 GCTGAATACC GGAGCGACCA CAAACGTAAC CAACGACAAC GTTACCGATG
501 ACGAGAAAAA ACGTGCGGCA AGCGTTAAAG ACGTATTAAA CGCTGGCTGG
551 AACATTAAAG GCGTTAAACC CGGTACAACA GCTTCCGATA ACGTTGATTT
601 CGTCCGCACT TACGACACAG TCGAGTTCTT GAGCGCAGAT ACGAAAACAA
651 CGACTGTAA TGTGGAAAGC AAAGACAACG GCAAGAAAAC CGAAGTTAAA
701 ATCGGTGCGA AGACTTCTGT TATTAAAGAA AAAGAC...
```

This corresponds to the amino acid sequence <SEQ ID 2; ORF40>:

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1  ..TLLFATVQAS ANQEEQEDL YLDPVQRTVA VLIVNSDKEG TGEKEKVEEN
51  SDWAVYFNEK GVLTAAREITX KAGDNLKIKQ NGTNFTYSLK KDLTDLTSVG
101 TEKLSFSANG NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDLT
151 LNTGATTNVT NDNVDDEKK RAASVKDVLN AGWNIKGVPK GTTASDNVDF
201 VRTYDTVEFL SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKD...
```

Further work revealed the complete DNA sequence <SEQ ID 3>:

```

1  ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCCTGGGT
51  CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
101 TGAAGACCGC CGTATTGGCG ACGTGTGT TTGCAACGGT TCAGGCAAGT
151 GCTAACAAATG AAGAGCAAGA AGAAGATTTA TATTAGACC CCGTACAACG
201 CACTGTTGCC GTGTTGATAG TCAATCCGA TAAAGAAGGC ACGGGAGAAA
251 AAGAAAAAGT AGAAGAAAAT TCAGATTGGG CAGTATATTT CAACGAGAAA
301 GGAGTACTAA CAGCCAGAGA AATCACCTC AAAGCCGGCG ACAACCTGAA
351 AATCAACAAA AACGGCACAA ACTTCACCTA CTCGCTGAAA AAAGACCTCA
401 CAGATCTGAC CAGTGTGGA ACTGAAAAAT TATCGTTTAG CGCAACGGC
451 AATAAAGTCA ACATCACAAG CGACACCAA GGCTTGAATT TTGCGAAAGA
501 AACGGCTGGG ACGAACGGCG ACACCACGGT TCATCTGAAC GGTATTGGTT
551 CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
601 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCGGCAA GCGTTAAAGA
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5 651 CGTATTAAAC GCTGGCTGGA ACATTAAAGG CGTTAAACCC GGTACAACAG
 701 CTTCCGATAA CGTTGATTTC GTCCGCACTT ACGACACAGT CGAGTTCCTG
 751 AGCGCAGATA CGAAAAACAAC GACTGTTAAT GTGGAAAGCA AAGACAACGG
 801 CAAGAAAACC GAAGTTAAAA TCGGTGCGAA GACTTCTGTT ATTAAAGAAA
 851 AAGACGGTAA GTTGGTTACT GGTAAAGACA AAGGCGAGAA TGGTCTTCT
 901 ACAGACGAAG GCGAAGGCTT AGTGACTGCA AAAGAAGTGA TTGATGCAGT
 951 AAACAAGGCT GGTGGAGAA TGAAAACAAC AACCGCTAAT GGTCAAACAG
 1001 GTCAAGCTGA CAAGTTTGAA ACCGTTACAT CAGGCACAAA TGTAACCTTT
 1051 GCTAGTGGTA AAGGTACAAC TGCGACTGTA AGTAAAGATG ATCAAGGCCAA
 1101 CATCACTGTT ATGTATGATG TAAATGTCGG CGATGCCCTA AACGTCAATC
 1151 AGCTGCAAAA CAGCGGTTGG AATTGGATT CCAAAGCGGT TGCAGGTTCT
 1201 TCGGGCAAAG TCATCAGCGG CAATGTTTCG CCGAGCAAGG GAAAGATGGA
 1251 TGAAACCGTC AACATTAATG CCGGCAACAA CATCGAGATT ACCCGCAACG
 1301 GTAAAAATAT CGACATCGCC ACTTCGATGA CCCCAGATT TTCCAGCGTT
 1351 TCGCTCGGCG CGGGGGCGGA TCGCGCCACT TTGAGCGTGG ATGGGGACGC
 1401 ATTGAATGTC GGCAGCAAGA AGGACAACAA ACCCGTCCGC ATTACCAATG
 1451 TCGCCCCGGG CGTTAAAGAG GGGGATGTTA CAAACGTCGC ACAACTTAAA
 1501 GGCGTGGCGC AAAACTTGAA CAACCGCATC GACAATGTGG ACGGCAACGC
 1551 GCGTGC GGCG ATCGCCCAAG CGATTGCAAC CGCAGGCTCG GTTCAGGCGT
 20 1601 ATTTGCCCGG CAAGAGTATG ATGGCGATCG GCGGCGGCAC TTATCGCGGC
 1651 GAAGCCGGTT ACGCCATCGG CTACTCCAGT ATTTCCGACG GCGGAAATTG
 1701 GATTATCAAA GGCACGGCTT CCGGCAATTC GCGCGGCCAT TTCGGTGCTT
 1751 CCGCATCTGT CGGTTATCAG TGGTAA

This corresponds to the amino acid sequence <SEQ ID 4; ORF40-1>:

25 1 MNKIYRIWN SALNAWVVVS ELTRNHTKRA SATVKTAFLA TLLFATVQAS
 51 ANNEEQEEDL YLDPVQRTVA VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
 101 GVLTAIREITL KAGDNLKIKQ NGTNFTYSLK KDLTDLTSVG TEKLSFSANG
 151 NKVNITSDTK GLNFAKETAG TNGDFTVHLN GIGSTLTDLT LNTGATTNVT
 201 NDNVTDDEKK RAASVKDVLN AGWNIKGVKP GTTASDNVDF VRTYDTVEFL
 30 251 SADTKTTTVN VESKDNKKKT EVKIGAKTSV IKEKDKGLVT GKDKGENGSS
 301 TDEGEGLVTA KEVIDAVNKA GWRMKT TAN GTGQADKFE TVTSGTNVTF
 351 ASGKGTATV SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
 401 SGKIGSNVS PSKGMDET V NINAGNNIEI TRNGKNIDIA TSMTPQFSSV
 451 SLGAGADAPT LSVGDALNV GSKKDNKPVR ITNVAPGVKE GDVTNVAQLK
 35 501 GVAQNLNNRI DNVGDGNARAG IAQAIATAGL VQAYLPGKSM MAIGGGTYRG
 551 EAGYAIGYSS ISDGGNWI K GTASGNSRGH FGASASVGYQ W*

Further work identified the corresponding gene in strain A of *N.meningitidis* <SEQ ID 5 >:

40 1 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCCTGNGT
 51 CGCCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG AACTGTGT TTGCAACGGT TCAGGCGAAT
 151 GCTACCGATG AAGATGAAGA AGAAGAGTTA GAATCCGTAC AACGCTCTGT
 201 CGTAGGGAGC ATTCAAGCCA GTATGGAAGG CAGCGGCGAA TTGGAAACGA
 251 TATCATTATC AATGACTAAC GACAGCAAGG AATTGTAGA CCCATACATA
 301 GTAGTTACCC TCAAAGCCGG CGACAACCTG AAAATCAAAC AAAACACCAA
 45 351 TGAAAACACC AATGCCAGTA GCTTACCTA CTCGTGAAA AAAGACCTCA
 401 CAGGCCTGAT CAATGTTGAN ACTGAAAAAT TATCGTTTGG CGCAAACGGC
 451 AAGAAAGTCA ACATCATAAG CGACACCAA GGCTGAATT TCGCGAAAGA
 501 AACGGCTGGG ACGAACGGCG ACACCACGGT TCATCTGAAC GGTATCGGTT
 551 CGACTTTGAC CGATACGCTT GCGGGTTCTT CTGCTTCTCA CGTTGATGCG
 50 601 GGTAACCNAA GTACACATTA CACTCGTGCA GCAAGTATTA AGGATGTGTT
 651 GAATGCGGGT TGGAAATATTA AGGGTGTTAA ANNNGGCTCA ACAACTGGTC
 701 AATCAGAAAA TGTCGATTTC GTCCGCACTT ACGACACAGT CGAGTTCCTG
 751 AGCGCAGATA CGNAAACAAC GACNGTTAAT GTGGAAAGCA AAGACAACGG
 801 CAAGAGAACC GAAGTTAAAA TCGGTGCGAA GACTTCTGTT ATTAAAGAAA
 55 851 AAGACGGTAA GTTGGTTACT GGTAAAGGCA AAGGCGAGAA TGGTCTTCT
 901 ACAGACGAAG GTTGAAGCTT AGTGACTGCA AAAGAAGTGA TTGATGCAGT
 951 AAACAAGGCT GGTGGAGAA TGAAAACAAC AACCGCTAAT GGTCAAACAG
 1001 GTCAAGCTGA CAAGTTTGAA ACCGTTACAT CAGGCACAAA TGTAACCTTT
 1051 GCTAGTGGTA AAGGTACAAC TGCGACTGTA AGTAAAGATG ATCAAGGCCAA
 60 1101 CATCACTGTT ATGTATGATG TAAATGTCGG CGATGCCCTA AACGTCAATC
 1151 AGCTGCAAAA CAGCGGTTGG AATTGGATT CCAAAGCGGT TGCAGGTTCT
 1201 TCGGGCAAAG TCATCAGCGG CAATGTTTCG CCGAGCAAGG GAAAGATGGA
 1251 TGAAACCGTC AACATTAATG CCGGCAACAA CATCGAGATT AGCCGCAACG
 1301 GTAAAAATAT CGACATCGCC ACTTCGATGG CCGCGCAGTT TTCCAGCGTT
 65 1351 TCGCTCGGCG CGGGGGCAGA TCGCGCCACT TTAAGCGTGG ATGACGAGGG
 1401 CGCGTTGAAT GTCGGCAGCA AGGATGCCAA CAAACCCGTC CGCATTACCA

1451 ATGTCGCCCC GGGCGTTAAA GANGGGGATG TTACAAACGT CNCACAACTT
 1501 AAAGGCGTGG CGCAAACTT GAACAACCGC ATCGACAATG TGGACGGCAA
 1551 CGCGCGTGCN GGCATCGCCC AAGCGATTGC AACCGCAGGT CTGGTTCCAGG
 1601 CGTATCTGCC CGGCAAGAGT ATGATGGCGA TCGGCGGCGG CACTTATCGC
 5 1651 GGCGAAGCCG GTTACGCCAT CGGCTACTCC AGTATTTCCG ACGGCGGAAA
 1701 TTGGATTATC AAAGGCACGG CTTCCGGCAA TTCGCGCGGC CATTTCGGTG
 1751 CTTCCGCATC TGTCGGTTAT CAGTGGTAA

This encodes a protein having amino acid sequence <SEQ ID 6; ORF40a>:

1 MNKIYRIWN SALNAXVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
 10 51 ATDEDEEEEL ESQVRSVGS IQASMEGSGE LETISLSMTN DSKEFVDPYI
 101 VVTLKAGDNL KIKQNTNENT NASSFTYSLK KDLTGLINVX TEKLSFGANG
 151 KKVNIISDTK GLNFAKETAG TNGDITVHLN GIGSTLTDL AGSSASHVDA
 201 GNXSTHYTRA ASIKDVLNAG WNIKGVKXGS TTGQSENVDF VRTYDTVEFL
 251 SADTXXTTVN VESKDNGKRT EVKIGAKTSV IKEKDGLVT GKKGENGSS
 15 301 TDEGEGLVTA KEVIDAVNKA GWRMKT TAN GQTGQADKFE TVTSGTNVTF
 351 ASGKGTTATV SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
 401 SGKVISGNVS PSKGKMDTV NINAGNNIEI SRNGKNIDIA TSMAPQFSSV
 451 SLGAGADAPT LSVDEGALN VGSKDANKPV RITNVAPGVK XGDVTNVXQL
 20 501 KGVAQNLNLR IDNVDGNARA GIAQAIATAG LVQAYLPGKS MMAIGGGTYR
 551 GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGY QW*

The originally-identified partial strain B sequence (ORF40) shows 65.7% identity over a 254aa overlap with ORF40a:

					10	20	30
25	orf40.pep				TLLFATVQASANQEEQEEEDLYLDPVQRTVA		
	orf40a	SALNAXVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL--ESQVRSV-					
		20	30	40	50	60	
30	orf40.pep	VLIVNSDKEGTGEKEKVEEN--SDWAVYFNEKGVLTAREITXKAGDNLKIKQN-----GT					
	orf40a	VGSIQASMEGSGELETISLSMTNDSKEFVDPYIV----VTLKAGDNLKIKQNTNENTNAS					
		70	80	90	100	110	120
35	orf40.pep	NFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITS DTKGLNFAKETAGTNGDITVHLNGIG					
	orf40a	SFTYSLKKDLTGLINVXTEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDITVHLNGIG					
		130	140	150	160	170	180
40	orf40.pep	STLTDITLLNTGATTNVTNDNVT DDEKKRAASVKDVLNAGWNIGVKPGTTA--SDNVDFV					
	orf40a	STLTDITLAGSSAS-HVDAGNXST-HYTRAASIKDVLNAGWNIGVKXGSGTTGQSENVDFV					
45		190	200	210	220	230	240
	orf40.pep	RTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKD					
	orf40a	RTYDTVEFLSADTXXTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGLVTGKKGENGSSST					
50		250	260	270	280	290	300

The complete strain B sequence (ORF40-1) and ORF40a show 83.7% identity in 601 aa overlap:

					10	20	30	40	50	60
55	orf40-1.pep	MNKIYRIWNSALNAWVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL								
	orf40a	MNKIYRIWNSALNAXVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL								
		10	20	30	40	50	60			
60	orf40-1.pep	YLDPVQRTVAVLIVNSDKEGTGEKEKVEEN--SDWAVYFNEKGVLTAREITLKAGDNLKIK								
		70	80	90	100	110	119			

	orf40a	--ESVQRSV-VGSIQASMEGSGSELETISLSMTNDSKEFVDPYIV----	VTLKAGDNLKIK
		70 80 90 100 110	
5	orf40-1.pep	120 130 140 150 160 170	
	orf40a	QNTNENTNASSFTYSLKKDLTGLINVTXTEKLSFGANGKKVNIISDTKGLNFAKETAGTNG	
10	orf40-1.pep	180 190 200 210 220 230	
	orf40a	DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIGVKPGT	
15	orf40-1.pep	240 250 260 270 280 290	
	orf40a	TGQSENVDFVRTYDTVEFLSADTXTTNNVESKDNKRTEVKIGAKTSVIKEKDGKLV	
20	orf40-1.pep	300 310 320 330 340 350	
	orf40a	KGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGQADKFETVTS	
25	orf40-1.pep	360 370 380 390 400 410	
	orf40a	SGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVIS	
30	orf40-1.pep	420 430 440 450 460 470	
	orf40a	SKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTL	
35	orf40-1.pep	480 490 500 510 520 530	
	orf40a	GSKKDANKPVRITNVAPGVKXGDTVNVXQLKGAQNLNLRIDNVDGNARAGIAQAI	
40	orf40-1.pep	540 550 560 570 580 590	
	orf40a	VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI	
45	orf40-1.pep	WX	
	orf40a	WX	

55 Computer analysis of these amino acid sequences gave the following results:

Homology with Hsf protein encoded by the type b surface fibrils locus of *H.influenzae*
(accession number U41852)

ORF40 and Hsf protein show 54% aa identity in 251 aa overlap:

60	Orf40	1	TLLFATVQASANQEEQEEDLYLDPVQRTVAVLIVNSDXXXXXXXXXXXXNSDWAVYFNEK	60
			TLLFATVQA+A E++E LDPV RT VL +SD NS+W +YF+ K	
	Hsf	41	TLLFATVQANATDEDEE----LDPVVRTAPVLSFHSKDKEGTGEKEVTE-NSNWGIYFDNK	95
65	Orf40	61	GVLTAAREITXKAGDNLKIKQN-----GTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVN	114
			GVL A IT KAGDNLKIKQN ++FTYSLKKDLTDLTSV TEKLSF ANG+KV+	
	Hsf	96	GVLKAGAITLKAGDNLKIKQNTDESTNASSFTYSLKKDLTDLTSVATEKLSFGANGDKVD	155

5 Orf40 115 ITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGAXXXXXXXXXXXXXEKKRAAS 174
 ITSD GL AK G+ VHLNG+ STL D + NTG EK RAA+
 Hsf 156 ITSDANGLKLAK-----TGNGNVHLNGLDSTLPDAVTNTGVLSSSSFTPNDV-EKTRAAT 209
 Orf40 175 VKDVLNAGWNIKGKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKI 234
 VKDVLNAGWNIKG K ++VD V Y+ VEF++ D T V + +K+NGK TEVK
 Hsf 210 VKDVLNAGWNIKGAKTAGGNVESVDLVSAYNNEFITGDKNTLDVVLTAKENGKTTTEVKF 269
 10 Orf40 235 GAKTSVIKEKD 245
 KTSVIKEKD
 Hsf 270 TPKTSVIKEKD 280

ORF40a also shows homology to Hsf:

15 gi|1666683 (U41852) hsf gene product [Haemophilus influenzae] Length = 2353
 Score = 153 (67.7 bits), Expect = 1.5e-116, Sum P(11) = 1.5e-116
 Identities = 33/36 (91%), Positives = 34/36 (94%)
 Query: 16 VAVSELTRNHTKRASATVKTAVLATLLFATVQANAT 51
 V VSELTR HTKRASATV+TAVLATLLFATVQANAT
 20 Sbjct: 17 VVSELTRTHTKRASATVETAVLATLLFATVQANAT 52
 Score = 161 (71.2 bits), Expect = 1.5e-116, Sum P(11) = 1.5e-116
 Identities = 32/38 (84%), Positives = 36/38 (94%)
 25 Query: 101 VTLKAGDNLKIKQNTNENTNASSFTYSLKKDLTGILNV 138
 +TLKAGDNLKIKQNT+E+TNASSFTYSLKKDLT L +V
 Sbjct: 103 ITLKAGDNLKIKQNTDESTNASSFTYSLKKDLTDLTSV 140
 Score = 110 (48.7 bits), Expect = 1.5e-116, Sum P(11) = 1.5e-116
 30 Identities = 21/29 (72%), Positives = 25/29 (86%)
 Query: 138 VTEKLSFGANGKKVNIISDTKGLNFAKET 166
 V++KLS G NG KVNI SDTKGLNFAK++
 35 Sbjct: 1439 VSDKLSLGTNGNKVNITSDTKGLNFAKDS 1467
 Score = 85 (37.6 bits), Expect = 1.5e-116, Sum P(11) = 1.5e-116
 Identities = 18/32 (56%), Positives = 20/32 (62%)
 40 Query: 169 TNGDTTVHLNGIGSTLTDTLAGSSASHVDAGN 200
 T D +HLNGI STLDTL S A+ GN
 Sbjct: 1469 TGDDANIHLNGIASTLTDTLLNSGATTNLGGN 1500
 Score = 92 (40.7 bits), Expect = 1.5e-116, Sum P(11) = 1.5e-116
 45 Identities = 16/19 (84%), Positives = 19/19 (100%)
 Query: 206 RAASIKDVLNAGWNIKGK 224
 RAAS+KDVLNAGWN++GVK
 Sbjct: 1509 RAASVKDVLNAGWNVRGVK 1527
 50 Score = 90 (39.8 bits), Expect = 1.5e-116, Sum P(11) = 1.5e-116
 Identities = 17/28 (60%), Positives = 20/28 (71%)
 Query: 226 STTGQSENVDFVRTYDTVEFLSADTTTT 253
 S Q EN+DFV TYDTV+F+S D TT
 55 Sbjct: 1530 SANNQVENIDFVATYDTVDFVSGDKDTT 1557

Based on homology with Hsf, it was predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

ORF40-1 (61kDa) was cloned in pET and pGex vectors and expressed in *E.coli*, as described above. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 1A shows the results of affinity purification of the His-fusion protein, and Figure 1B shows the

results of expression of the GST-fusion in *E. coli*. Purified His-fusion protein was used to immunise mice, whose sera were used for FACS analysis (Figure 1C), a bactericidal assay (Figure 1D), and ELISA (positive result). These experiments confirm that ORF40-1 is a surface-exposed protein, and that it is a useful immunogen.

5 Figure 1E shows plots of hydrophilicity, antigenic index, and AMPHI regions for ORF40-1.

Example 2

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 7>

```

10      1  ATGTTACGTT TGACTGCTTT AGCCGTATGC ACCGCCCTCG CTTTGGGCGC
      51  GTGTTCCGCG CAAAATTCCG ACTCTGCCCC ACAAGCCAAA GaACAGGCGG
      101  TTTCCGCGCG ACAAACCGAA GgCGCGTCCG TTACCGTCAA AACCgCGCGC
      151  GCGGACGTTT AAATACCGCA AAACCCCGAA CGCATCGCCG TTTACGATTT
      201  GGGTATGCTC GACACCTTGA GCAAACCTGGG CGTGAAAACC GGTTTGTCGG
      251  TCGATAAAAA CCGCCTGCCG TATTTAGAGG AATATTTCAA AACGACAAAA
      301  CCTGCCGGCA CTTTGTTTGA GCCGGATTAC GAAACGCTCA ACGCTTACAA
      351  ACCGCAGCTC ATCATCATCG GCAGCCGCGC CgCCAAGGCG TTTGACAAAT
      401  TGAACGAAAT CGCGCCGACC ATCGrmwTGA CCGCGATAC CGCCAACCTC
      451  AAAGAAAGTG CCAArGAGGC ATCGACGCTG GCGCAAATCT TC..

```

This corresponds to the amino acid sequence <SEQ ID 8; ORF38>:

```

20      1  MLRLTALAVC TALALGACSP QNSDSAPQAK EQAVSAAQTE GASVTVKTAR
      51  GDVQIPQNPE RIAVYDLGML DTLsklgvkt GLSVdKNRLP YLEEFKTTK
      101  PAGTLFEPDY ETLNAYKPQL IIIGSRAAKA FDKLNEIAPT IXXTADTANL
      151  KESAKEASTL AQIF..

```

Further work revealed the complete nucleotide sequence <SEQ ID 9>:

```

25      1  ATGTTACGTT TGACTGCTTT AGCCGTATGC ACCGCCCTCG CTTTGGGCGC
      51  GTGTTCCGCG CAAAATTCCG ACTCTGCCCC ACAAGCCAAA GAACAGGCGG
      101  TTTCCGCGCG ACAAACCGAA GGCGCGTCCG TTACCGTCAA AACCgCGCGC
      151  GCGGACGTTT AAATACCGCA AAACCCCGAA CGCATCGCCG TTTACGATTT
      201  GGGTATGCTC GACACCTTGA GCAAACCTGGG CGTGAAAACC GGTTTGTCGG
      251  TCGATAAAAA CCGCCTGCCG TATTTAGAGG AATATTTCAA AACGACAAAA
      301  CCTGCCGGCA CTTTGTTTGA GCCGGATTAC GAAACGCTCA ACGCTTACAA
      351  ACCGCAGCTC ATCATCATCG GCAGCCGCGC CGCCAAGGCG TTTGACAAAT
      401  TGAACGAAAT CGCGCCGACC ATCGAAATGA CCGCCGATAC CGCCAACCTC
      451  AAAGAAAGTG CCAAAGAGCG CATCGACGCG CTGGCGCAAA TCTTCGGCAA
      501  ACAGGCGGAA GCCGACAAGC TGAAGGCGGA AATCGACGCG TCTTTTGAAG
      551  CCGCGAAAAC TGCCGCACAA GGTAAGGGCA AAGGTTTGGT GATTTTGGTC
      601  AACGGCGGCA AGATGTCGGC TTTCGGCCCG TCTTCACGCT TGGGCGGCTG
      651  GCTGCACAAA GACATCGGCG TTCCCGCTGT CGATGAATCA ATTAAAGAAG
      701  GCAGCCACGG TCAGCCTATC AGCTTTGAAT ACCTGAAAGA GAAAAATCCC
      751  GACTGGCTGT TTGTCTTGA CCGAAGCGCG GCCATCGGCG AAGAGGGTCA
      801  GGCGGCGAAA GACGTGTTGG ATAATCCGCT GGTGCGGAA ACAACCGCTT
      851  GGAAAAAAGG ACAGGTCGTG TACCTCGTTC CTGAACTTA TTTGGCAGCC
      901  GGTGGCGCGC AAGAGCTGCT GAATGCAAGC AAACAGGTTG CCGACGCTTT
      951  TAACGCGGCA AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 10; ORF38-1>:

```

45      1  MLRLTALAVC TALALGACSP QNSDSAPQAK EQAVSAAQTE GASVTVKTAR
      51  GDVQIPQNPE RIAVYDLGML DTLsklgvkt GLSVdKNRLP YLEEFKTTK
      101  PAGTLFEPDY ETLNAYKPQL IIIGSRAAKA FDKLNEIAPT IEMTADTANL
      151  KESAKERIDA LAQIFGKQAE ADKLKAEIDA SFEAAKTAQ GKgKGLVILV
      201  NGGKMFAFGP SSRLGGWLHK DIGVPAVDES IKEGSHGQPI SFEYLKEKNP
      50  251  DWLFVLDRSA AIGEEGQAAK DVLdNPLVAE TTAWKKGQVV YLVPETYLA

```


301 GGAQELLNAS KQVADAFNAA K*

Computer analysis of this amino acid sequence reveals a putative prokaryotic membrane lipoprotein lipid attachment site (underlined).

Further work identified the corresponding gene in strain A of *N.meningitidis* <SEQ ID 11>:

```

5      1  ATGTTACGTT  TGA CTGCTTT  AGCCGTATGC  ACCGCCCTCG  CTTTGGGCGC
      51  GTGTTGCGCG  CAAATATCCG  ACTCTGCCCC  ACAAGCCAAA  GAACAGGCGG
     101  TTTCCGCGCG  ACAATCCGAA  GGCCTGTCCG  TTACCGTCAA  AACGGCGCGC
     151  GGCGATGTTT  AAATACCGCA  AAACCCGAA  CGTATCGCCG  TTTACGATTT
     201  GGGTATGCTC  GACACCTTGA  GCAAACGCG  CGTGAAACC  GGTTGTCCG
    10  251  TCGATAAAAA  CCGCTGCGG  TATTTAGAGG  AATATTTCAA  AACGACAAAA
     301  CCTGCCGGA  CTTGTTCGA  GCCGATTAC  GAAACGCTCA  ACGCTTACAA
     351  ACCGCAGCTC  ATCATCATCG  GCAGCCGCG  AGCCAAAGCG  TTTGACAAAT
     401  TGAACGAAAT  CGCGCCGACC  ATCGAAATGA  CCGCCGATAC  CGCCAACCTC
     451  AAAGAAAGTG  CCAAAGAGCG  TATCGACGCG  CTGGCGCAA  TCTTCGCAA
    15  501  AAAGGCGGAA  GCCGACAAGC  TGAAGGCGGA  AATCGACGCG  TCTTTTGAAG
     551  CCGCGAAAC  TGCCGCGCAA  GGCAAAGGCA  AGGGTTTGGT  GATTTTGGTC
     601  AACGGCGGCA  AGATGTCCGC  CTTCGGCCCG  TCTTCACGAC  TGGGCGGCTG
     651  GCTGCACAAA  GACATCGGCG  TTCCCGCTGT  TGACGAAGCC  ATCAAAGAAG
    20  701  GCAGCCACGG  TCAGCCTATC  AGCTTTGAAT  ACCTGAAAGA  GAAAAATCCC
     751  GACTGGCTGT  TTGTCCTTGA  CCGCAGCGCG  GCCATCGGCG  AAGAGGGTCA
     801  GGCGGCGAAA  GACGTGTTGA  ACAATCCGCT  GGTGCGCGAA  ACAACCGCTT
     851  GGAAAAAAG  ACAAGTCGTT  TACCTTGTTT  CTGAACTTA  TTTGGCAGCC
     901  GGTGGCGCG  AAGAGCTACT  GAATGCAAGC  AAACAGGTTG  CCGACGCTTT
     951  TAACGCGGCA  AAATAA
  
```

25 This encodes a protein having amino acid sequence <SEQ ID 12; ORF38a>:

```

      1  MLRLTALAVC  TALALGACSP  QNSDSAPQAK  EQAVSAAQSE  GVSVTVK TAR
     51  GDVQIPQNPE  RIAVYDLGML  DTL SKLGVKT  GLSVDKNR LP  YLEEFKTTK
    101  PAGTLFEPDY  ETLNAYKPQL  IIIGSRAAKA  FDKLNEIAPT  IEMTADTANL
    151  KESAKERIDA  LAQIFGKKA E  ADKLKAEIDA  SFEAAKTAAQ  GKKGGLVILV
    201  NGGKMSAFGP  SSRLGGWLHK  DIGVPAVDEA  IKEGSHGQPI  SFEYLKEKNP
    251  DWLFVLDRSA  AIGEEGQAAK  DVLNNPLVAE  TTAWKKGQV  YLVPETYLAA
    301  GGAQELLNAS  KQVADAFNAA  K*
  
```

The originally-identified partial strain B sequence (ORF38) shows 95.2% identity over a 165aa overlap with ORF38a:

```

35      10      20      30      40      50      60
    orf38.pep  MLRLTALAVCTALALGACSPQNSDSAPQAKEQAVSAAQTEGASVTVK TARGDVQIPQNPE
    orf38a     MLRLTALAVCTALALGACSPQNSDSAPQAKEQAVSAAQSEGVSVTVKTARGDVQIPQNPE
      10      20      30      40      50      60
    40      70      80      90      100     110     120
    orf38.pep  RIAVYDLGMLDTLSKLGVTGLSVDKNR LPYLEEFKTTK PAGTLFEPDYETLNAYKPQL
    orf38a     RIAVYDLGMLDTLSKLGVTGLSVDKNR LPYLEEFKTTK PAGTLFEPDYETLNAYKPQL
    45      70      80      90      100     110     120
      130     140     150     160
    orf38.pep  IIIGSRAAKAFDKLNEIAPTIXXTADTANLKESAKE-ASTLAQIF
    orf38a     IIIGSRAAKAFDKLNEIAPTIEMTADTANLKESAKERIDALAQIFGKKA EADKLKAEIDA
      130     140     150     160     170     180
    orf38a     SFEAAKTAAQGGKGLVILVNGGKMSAFGPSSRLGGWLHKDIGVPAVDEAIKEGSHGQPI
      190     200     210     220     230     240
  
```

55 The complete strain B sequence (ORF38-1) and ORF38a show 98.4% identity in 321 aa overlap:

```

    orf38a.pep    MLRLTALAVCTALALGACSPQNSDSAPQAKEQAVSAAQSEGVSVTVKTARGDVQIPQNPE
    orf38-1       MLRLTALAVCTALALGACSPQNSDSAPQAKEQAVSAAQTEGASVTVKTARGDVQIPQNPE
5   orf38a.pep    RIAVYDLGMLDTLSKLGVKTGLSVDKNRLPYLEEYFKTTKPAGTLFEPDYETLNAYKPQL
    orf38-1       RIAVYDLGMLDTLSKLGVKTGLSVDKNRLPYLEEYFKTTKPAGTLFEPDYETLNAYKPQL
10  orf38a.pep    I I I G S R A A K A F D K L N E I A P T I E M T A D T A N L K E S A K E R I D A L A Q I F G K K A E A D K L K A E I D A
    orf38-1       I I I G S R A A K A F D K L N E I A P T I E M T A D T A N L K E S A K E R I D A L A Q I F G K Q A E A D K L K A E I D A
15  orf38a.pep    S F E A A K T A A Q G K G K L V I L V N G G K M S A F G P S S R L G G W L H K D I G V P A V D E A I K E G S H G Q P I
    orf38-1       S F E A A K T A A Q G K G K L V I L V N G G K M S A F G P S S R L G G W L H K D I G V P A V D E S I K E G S H G Q P I
20  orf38a.pep    S F E Y L K E K N P D W L F V L D R S A A I G E E G Q A A K D V L N N P L V A E T T A W K K G Q V V Y L V P E T Y L A A
    orf38-1       S F E Y L K E K N P D W L F V L D R S A A I G E E G Q A A K D V L N N P L V A E T T A W K K G Q V V Y L V P E T Y L A A
    orf38a.pep    G G A Q E L L N A S K Q V A D A F N A A K
    orf38-1       G G A Q E L L N A S K Q V A D A F N A A K

```

Computer analysis of these sequences revealed the following:

25 Homology with a lipoprotein (lipo) of *C.jejuni* (accession number X82427)

ORF38 and lipo show 38% aa identity in 96 aa overlap:

```

    Orf38: 40  EGASVTVKTARGDVQIPQNPERIAVYDLGMLDTLSKLGVKTGLS-VDKNRLPYLEEYFKT 98
                EG S  VK + G+ + P+NP ++ + DLG+LDT  L +  ++ V  LP  + FK
30  Lipo:  51  EGDSFLVKDSLGENKTPKNPSKVVILDGLDITFDALKLNDKVAGVPAKNLPKYLQQFKN 110
    Orf38: 99  TKPAGTLFEPDYETLNAYKPQLIIIGSRAAKAFDKL 134
                G + + D+E +NA KP LIII  R +K +DKL
    Lipo:  111 KPSVGGVQQVDFEAINALKPDLIIISGRQSKFYDKL 146

```

Based on this analysis, it was predicted that this protein from *N.meningitidis*, and its epitopes, could
 35 be useful antigens for vaccines or diagnostics.

ORF38-1 (32kDa) was cloned in pET and pGex vectors and expressed in *E.coli*, as described above. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification of the His-fusion protein, and Figure 2B shows the results of expression of the GST-fusion in *E.coli*. Purified His-fusion protein was used to immunise
 40 mice, whose sera were used for Western blot analysis (Figure 2C) and FACS analysis (Figure 2D). These experiments confirm that ORF38-1 is a surface-exposed protein, and that it is a useful immunogen.

Figure 2E shows plots of hydrophilicity, antigenic index, and AMPHI regions for ORF38-1.

Example 3

45 The following *N.meningitidis* DNA sequence was identified <SEQ ID 13>:

```

1  ATGAAACTTC TGACCACCGC AATCCTGTCT TCCGCAATCG CGCTCAGCAG
51 TATGGCTGCC GCCGCTGGCA CGGACAACCC CACTGTTGCA AAAAAAACCG
101 TCAGCTACGT CTGCCAGCAA GGTAAAAAAG TCAAAGTAAC CTACGGCTTC
151 AACAAACAGG GTCTGACCAC ATACGCTTCC GCCGTCATCA ACGGCAAACG
201 CGTGCAAATG CCTGTCAATT TGGACAAATC CGACAATGTG GAAACATTCT
251 ACGGCAAAGA AGGCGGTTAT GTTTTGGGTA CCGGCGTGAT GGATGGCAAA
301 TCCTACCGCA AACAGCCCAT TATGATTACC GCACCTGACA ACCAAATCGT
351 CTTCAAAGAC TGTTCCCCAC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 14; ORF44>:

```

10 1  MKLLTTAILS SAIALSSMAA AAGTDNPTVA KKTVSIVCQQ GKKVKVITYGF
51  NKQGLTTYAS AVINGKRVQM PVNLDKSDNV ETFYGKEGGY VLGTGVMDGK
101 SYRKQPIMIT APDNQIVFKD CSPR*

```

Computer analysis of this amino acid sequence predicted the leader peptide shown underlined.

Further work identified the corresponding gene in strain A of *N.meningitidis* <SEQ ID 15>:

```

15 1  ATGAAACTTC TGACCACCGC AATCCTGTCT TCCGCAATCG CGCTCAGCAG
51  TATGGCTGCT GCTGCCGGCA CGAACAACCC CACCGTTGCC AAAAAAACCG
101 TCAGCTACGT CTGCCAGCAA GGTAAAAAAG TCAAAGTAAC CTACGGCTTT
151 AACAAACAGG GCCTGACCAC ATACGCTTCC GCCGTCATCA ACGGCAAACG
201 TGTGCAAATG CCTGTCAATT TGGACAAATC CGACAATGTG GAAACATTCT
20 251 ACGGCAAAGA AGGCGGTTAT GTTTTGGGTA CCGGCGTGAT GGATGGCAAA
301 TCCTATCGCA AACAGCCTAT TATGATTACC GCACCTGACA ACCAAATCGT
351 CTTCAAAGAC TGTTCCCCAC GTTAA

```

This encodes a protein having amino acid sequence <SEQ ID 16; ORF44a>:

```

25 1  MKLLTTAILS SAIALSSMAA AAGTNNPTVA KKTVSIVCQQ GKKVKVITYGF
51  NKQGLTTYAS AVINGKRVQM PVNLDKSDNV ETFYGKEGGY VLGTGVMDGK
101 SYRKQPIMIT APDNQIVFKD CSPR*

```

The strain B sequence (ORF44) shows 99.2% identity over a 124aa overlap with ORF44a:

```

30 orf44.pep  10      20      30      40      50      60
      MKLLTTAILSSAIALSSMAAAAGTDNPTVAKKTVSYVCQQGKKVKVITYGFNKQGLTTYAS
      |||
orf44a      MKLLTTAILSSAIALSSMAAAAGTNNPTVAKKTVSYVCQQGKKVKVITYGFNKQGLTTYAS
      10      20      30      40      50      60

35 orf44.pep  70      80      90      100     110     120
      AVINGKRVQMPVNLDKSDNVETFYGKEGGYVLGTGVMDGKSYRKQPIMITAPDNQIVFKD
      |||
orf44a      AVINGKRVQMPVNLDKSDNVETFYGKEGGYVLGTGVMDGKSYRKQPIMITAPDNQIVFKD
      70      80      90      100     110     120

40 orf44.pep  CSPRX
      ||||
orf44a      CSPRX

```

Computer analysis gave the following results:

Homology with the LecA adhesin of *Eikenella corrodens* (accession number D78153)

45 ORF44 and LecA protein show 45% aa identity in 91 aa overlap:

```

Orf44  33  TVSYVCQQGKKVKVITYGFNKQGLTTYASAVINGKRVQMPVNLDKSDNVETFYGKEGGYVL 92
      +V+YVCQQG+++ V Y FN  G+ T A  +N + +++P NL  SDNV+T +   GY L
LecA   135 SVAYVCQQGRRNLNVNYRFNSAGVPTSaelrvnnrnlrlpynlsasdnvdtvf-SANGYRL 193

50 Orf44  93  GTGVMDGKSYRKQPIMITAPDNQIVFKDCSP 123
      T  MD  +YR Q I+++AP+  Q+++KDCSP

```

LecA 194 TTNAMDSANYRSQDIIVSAPNGQMLYKDCSP 224

Based on homology with the adhesin, it was predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

ORF44-1 (11.2kDa) was cloned in pET and pGex vectors and expressed in *E.coli*, as described above. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification of the His-fusion protein, and Figure 3B shows the results of expression of the GST-fusion in *E.coli*. Purified His-fusion protein was used to immunise mice, whose sera were used for ELISA, which gave positive results, and for a bactericidal assay (Figure 3C). These experiments confirm that ORF44-1 is a surface-exposed protein, and that it is a useful immunogen.

Figure 3D shows plots of hydrophilicity, antigenic index, and AMPHI regions for ORF44-1.

Example 4

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 17>

```

15      1  ..GGCACCGAAT TCAAAACCAC CCTTTCGGGA GCCGACATAC AGGCAGGGGT
      51  GGGTGAAAAA GCCCGAGCCG ATGCGAAAAT TATCCTAAAA GGCATCGTTA
     101  ACCGCATCCA AACC GAAGAA AAGCTGGAAT CCAACTCGAC CGTATGGCAA
     151  AAGCAGGCCG GAAGCGGCAG CACGGTTGAA ACGCTGAAGC TACCGAGCTT
     201  TGAAGGGCCG GCACTGCCTA AGCTGACCGC TCCCGGCGGC TATATCGCCG
     251  ACATCCCCAA AGGCAACCTC AAAACCGAAA TCGAAAAGCT GGCCAAACAG
     301  CCCGAATATG CCTATCTGAA ACAGCTTCAG ACGGTCAAGG ACGTGAAGT
     351  GAACCAAGTA CAGCTCGCTT ACGACAAATG GGAATAATAA CAGGAAGGCC
     401  TAACCGGAGC CGGAGCCGCA ATTANCGCAC TGGCCGTTAC CGTGGTCACC
     451  TCAGGCGCAG GAACCGGAGC CGTATTGGGA TTAANACNGT TGGCCGCCGC
     501  CGCAACCGAT GCAGCATTT...

```

25 This corresponds to the amino acid sequence <SEQ ID 18; ORF49>:

```

      1  ..GTEFKTTLSG ADIQAGVGEK ARADAKIILK GIVNRIQTEE KLESNSTVWQ
     51  KQAGSGSTVE TLKLPSEFGP ALPKLTAPGG YIADIPKGNL KTEIEKLAKQ
    101  PEYAYLKQLQ TVKDVNWNQV QLAYDKWDYK QEGLTGAGAA IXALAVTVVT
    151  SGAGTGAVLG LXRVAATAAD AAF..

```

30 Further work revealed the complete nucleotide sequence <SEQ ID 19>:

```

      1  ATGCAACTGC TGGCAGCCGA AGGCATTCAC CAACACCAAT TGAATGTTC
     51  GAAAAGTACC CGTTTCATCG GCATCAAAGT GGGTAAAAGC AATTACAGCA
    101  AAAACGAGCT GAACGAAACC AACTGCCCG TACGCGTTAT CGCCCAAACA
    151  GCCAAACCC GTTCCGCTG GGATACCGTA CTCGAAGGCA CCGAATTCAA
    201  AACCACCCTT TCCGGAGCCG ACATACAGGC AGGGGTGGGT GAAAAGCCC
    251  GAGCCGATGC GAAAATTATC CTAAGGCA TCGTTAACCG CATCCAAACC
    301  GAAGAAAAGC TGGAAATCAA CTCGACCGTA TGGCAAAAGC AGGCCGAAG
    351  CGGCAGCACG GTTGAAACGC TGAAGCTACC GAGCTTGAA GGGCCGCAC
    401  TGCCTAAGCT GACCGTCCC GCGGCTATA TCGCCGACAT CCCCAGGCG
    451  AACCTCAAAA CCGAATCGA AAAGTGGCC AACAGCCCCG AATATGCCTA
    501  TCTGAAACAG CTTAGACGG TCAAGGACGT GAACTGGAAC CAAGTACAGC
    551  TCGCTTACGA CAAATGGGAC TATAACAGG AAGGCCTAAC CGGAGCCGGA
    601  GCCGCAATTA TCGCACTGGC CGTTACCGTG GTCACCTCAG GCGCAGGAAC
    651  CGGAGCCGTA TTGGATTAA ACGGTGCGGC CGCCGCCGCA ACCGATGCAG

```

701 CATTTGCCTC TTTGGCCAGC CAGGCTTCCG TATCGTTCAT CAACAACAAA
 751 GGCAATATCG GTAACACCCT GAAAGAGCTG GGCAGAAGCA GCACGGTGAA
 801 AAATCTGATG GTTGGCGTCG CTACCGCAGG CGTAGCCGAC AAAATCGGTG
 851 CTTCGGCACT GAACAATGTC AGCGATAAGC AGTGGATCAA CAACCTGACC
 901 GTCAACCTGG CCAATGCGGG CAGTGCCGCA CTGATTAATA CCGCTGTCAA
 951 CGGCGGCAGC CTGAAAGACA ATCTGGAAGC GAATATCCTT GCGGCTTTGG
 1001 TGAATACTGC GCATGGAGAG GCAGCAAGTA AAATCAAACA GTTGGATCAG
 1051 CACTACATTG CCCATAAGAT TGCCCATGCC ATAGCGGGCT GTGCGGCAGC
 1101 GGCAGCGAAT AAGGGCAAGT GTCAAGATGG TGCATCGGT GCGGCGGTGCG
 1151 GTGAAATCCT TGGCGAAACC CTAATGGACG GCAGAGACCC TGGCAGCCTG
 1201 AATGTGAAGG ACAGGGCAAA AATCATTGCT AAGGCGAAGC TGGCAGCAGG
 1251 GGCAGTTGCG GCGTTGAGTA AGGGGGATGT GAGTACGGCG GCGAATGCGG
 1301 CTGCTGTGGC GGTAGAGAAT AATTCTTTAA ATGATATACA GGATCGTTTG
 1351 TTGAGTGGAA ATTATGCTTT ATGTATGAGT GCAGGAGGAG CAGAAAGCTT
 1401 TTGTGAGTCT TATCGACCAC TGGGCTTGCC ACACTTTGTA AGTGTTCAG
 1451 GAGAAATGAA ATTACCTAAT AAATTCGGGA ATCGTATGGT TAATGGAAAA
 1501 TTAATTATTA AACTAGAAA TGGCAATGTA TATTTCTCTG TAGGTAAAT
 1551 ATGGAGTACT GTAAATCAA CAAAATCAA TATAAGTGGG GTATCTGTCG
 1601 GTTGGGTTTT AAATGTTTCC CCTAATGATT ATTTAAAAGA AGCATCTATG
 1651 AATGATTCA GAAATAGTAA TCAAATAAA GCCTATGCAG AAATGATTTT
 1701 CCAGACTTTG GTAGGTGAGA GTGTTGGTGG TAGTCTTTGT CTGACAGAG
 1751 CCTGCTTTTC GGTAAGTTCA ACAATATCTA AATCTAAATC TCCTTTTAAA
 1801 GATTCAAAAA TTATTGGGGA AATCGGTTTG GGAAGTGGTG TTGCTGCAGG
 1851 AGTAGAAAAA ACAATATACA TAGGTAACAT AAAAGATATT GATAAATTTA
 1901 TTAGTGCAAA CATAAAAAA TAG

This corresponds to the amino acid sequence <SEQ ID 20; ORF49-1>:

1 MQLLAAEGIH QHQLNVQKST RFIGIKVGKS NYSKNELNET KLPVRVIAQT
 51 AKTRSGWDTV LEGTEFKTTL SGADIQAGVG EKARADAKII LKGIVNRIQT
 101 EEKLESNSTV WQKQAGSGST VETLKLPSFE GPALPKLTAP GGYIADIPKG
 151 NLKTEIEKLA KQPEYAYLKQ LQTVKDVNWN QVQLAYDKWD YKQEGLTGAG
 201 AAIIALAVTV VTSGAGTGAV LGLNGAAAAA TDAAFASLAS QASVSFINNK
 251 GNIGNTLKEL GRSSTVKNLM VAVATAGVAD KIGASALNNV SDKQWINNLT
 301 VNLANAGSAA LINTAVNGGS LKDNLEANIL AALVNTAHGE AASKIKQLDQ
 351 HYIAHKIAHA IAGCAAAAAN KGKQDGAIG AAVGEILGET LLDGRDPGSL
 401 NVKDRAKIIA KAKLAAGAVA ALSKGDVSTA ANAAVAVEN NSLNDIQDRL
 451 LSGNYALCMS AGGAESFCES YRPLGLPHFV SVSGEMKLPN KFGNRMVNGK
 501 LIINTRNGNV YFSVGKIWST VKSTKSNISG VSVGWVLNVS PNDYLKEASM
 551 NDFRNSNQNK AYAEMISQTL VGESVGGSLC LTRACFSVSS TISKSKSPFK
 601 DSKIIGEIGL GSGVAAGVEK TIYIGNIKDI DKFISANIKK *

40 Computer analysis predicts a transmembrane domain and also indicates that ORF49 has no significant amino acid homology with known proteins. A corresponding ORF from *N.meningitidis* strain A was, however, identified:

ORF49 shows 86.1% identity over a 173aa overlap with an ORF (ORF49a) from strain A of *N.meningitidis*:

45 orf49.pep GTEFKTTLSGADIQAGVGEKARADAKIILK
 orf49a SKNELNETKLPVRVVAQXAATRSWDTVLEGTEFKTTLAGADIQAGVXEKARVDAKIILK
 50 orf49.pep GIVNRIQTEEKLESNSTVWQKQAGSGSTVETLKLPSFEGPALPKLTAPGGYIADIPKGNL
 orf49a GIVNRIQSEEKLETNSTVWQKQAGRGSTIETLKLPSFESPTPPKLSAPGGYIVDIPKGNL
 55 orf49.pep KTEIEKLAKQPEYAYLKQLQTVKDVNWNQVQLAYDKWDYKQEGLTGAGAAIXALAVTVVT

orf49a	KTEIEKLSKQPEYAYLKQLQVAKNINWNQVQLAYDRWDYKQEGLTEAGAAIIALAVTVVT
	160 170 180 190 200 210
5 orf49.pep	SGAGTGAVLGLXRVAATAAF
	160 170
orf49a	SGAGTGAVLGLNGAXAAATDAAFASLASQASVSFINNKGDVGKTLKELGRSSTVKNLVVA
	220 230 240 250 260 270

ORF49-1 and ORF49a show 83.2% identity in 457 aa overlap:

10	orf49a.pep	XQLLAEEGIHKHELDVQKSRFIGIKVGXSNYSKNELNETKLPVRVVAQXAATRSWDTV
	orf49-1	MQLLAEEGIHQHQLNVQKSTRFIGIKVGXSNYSKNELNETKLPVRVIAQTAKTRSGWDTV
15	orf49a.pep	LEGTEFKTTLGADIQAGVXEKARVDAKIILKGIVNRIQSEEKLETNSTVWQKQAGRGST
	orf49-1	LEGTEFKTTLGADIQAGVGEKARADAKIILKGIVNRIQTEEKLESNSTVWQKQAGSGST
20	orf49a.pep	IETLKLPSFESPTPPKLSAPGGYIVDIPKGNLKTEIEKLSKQPEYAYLKQLQVAKNINWN
	orf49-1	VETLKLPSFEGPALPKLTAPGGYIADIPKGNLKTEIEKLAKQPEYAYLKQLQTVKDVNWN
25	orf49a.pep	QVQLAYDRWDYKQEGLTEAGAAIIALAVTVVTSGAGTGAVLGLNGAXAAATDAAFASLAS
	orf49-1	QVQLAYDKWDYKQEGLTGAGAAIIALAVTVVTSGAGTGAVLGLNGAAAAATDAAFASLAS
30	orf49a.pep	QASVSFINNKGDVGKTLKELGRSSTVKNLVVAAATAGVADKIGASALXNVSDKQWINNLT
	orf49-1	QASVSFINNKGNIQNTLTLKELGRSSTVKNLMVAVATAGVADKIGASALNNVSDKQWINNLT
35	orf49a.pep	VNLNAGSAAALINTAVNGGSLKDXLEANILAALVNTAHGEAASKIKQLDQHYIVHKIAHA
	orf49-1	VNLNAGSAAALINTAVNGGSLKDNLEANILAALVNTAHGEAASKIKQLDQHYIAHKIAHA
40	orf49a.pep	IAGCAAAAANKGKCQDGAIGAAGVEIVGEALTNGKNPDTLTAKEREQILAYSKLVAGTVS
	orf49-1	IAGCAAAAANKGKCQDGAIGAAGVEILGETLLDGRDPGSLNVKDKAKIIAKAKLAAGAVA
	orf49a.pep	GVVGGDVNAAANAEEVAVKNNQLSDXEGREFDNEMTACAKQNXPLCRKNTVKKYQNVAD
	orf49-1	ALSKGDVSTAANAAAVAVENNSLNDIQDRLLSGNYALCMSAGGAESFCESYRPLGLPHFV
	orf49a.pep	KRLAASIAICTDISRSTECRTIRKQHLIDSRSLHSSWEAGLIGKDDWEYKLFKSYTQAD
	orf49-1	SVSGEMKLPNKFGRNMVNGKLIINTRNGNVYFSVGKIWSTVKSTKSNISGVSVGWVLNVS

45 The complete length ORF49a nucleotide sequence <SEQ ID 21> is:

1	NTGCAACTGC	TGGCAGAAGA	AGGCATCCAC	AAGCACGAGT	TGGATGTCCA
51	AAAAAGCCGC	CGCTTTATCG	GCATCAAGGT	AGGTNAGAGC	AATTACAGTA
101	AAACGAACT	GAACGAAACC	AAATTCGCTG	TCCGCGTCGT	CGCCCAAANT
151	GCAGCCACCC	GTTACGGCTG	GGATACCGTG	CTCGAAGGTA	CCGAATTCAA
201	AACCACGCTG	GCCGGTGCCG	ACATTACGGC	AGGTGTANGC	GAAAAAGCCC
251	GTGTCGATGC	GAAAATTATC	CTCAAAGGCA	TTGTGAACCG	TATCCAGTCG
301	GAAGAAAAAT	TAGAAACCAA	CTCAACCGTA	TGGCAGAAAC	AGGCCGGACG
351	CGGCAGCACT	ATCGAAACGC	TAAACTGCC	CAGCTTCGAA	AGCCCTACTC
401	CGCCCAAATT	TTCGCGACCC	GGCGGNTATA	TCGTCGACAT	TCCGAAAGGC
451	AATCTGAAAA	CCGAAATCGA	AAAGCTGTCC	AAACAGCCCG	AGTATGCCTA
501	TCTGAAACAG	CTCCAAGTAG	CGAAAAACAT	CAACTGGAAT	CAGGTGCAGC
551	TTGCTTACGA	CAGATGGGAC	TACAAACAGG	AGGGCTTAAC	CGAAGCAGGT
601	GCGGCGATTA	TCGCACTGGC	CGTTACCGTG	GTCACTCAG	GCGCAGGAAC
651	CGGAGCCGTA	TTGGGATTAA	ACGGTGCNG	CGCCGCCGCA	ACCGATGCAG
701	CATTGCGCTC	TTTGCCGAGC	CAGGCTTCCG	TATCGTTTAT	CAACAACAAA
751	GGCGATGTCT	GCAAAACCTT	GAAAGAGCTG	GGCAGAAGCA	GCACGGTGAA
801	AAATCTGGTG	GTTGCCGCCG	CTACCGCAGG	CGTAGCCGAC	AAAATCGGCG
851	CTTCGGCACT	GANCAATGTC	AGCGATAAGC	AGTGGATCAA	CAACCTGACC
901	GTCAACCTAG	CCAATGCGGG	CAGTGCCGCA	CTGATTAATA	CCGCTGTCAA
951	CGGCGGCAGC	CTGAAAGACA	NTCTGGAAGC	GAATATCCTT	GCGGCTTTGG
1001	TCAATACCGC	GCATGGAGAA	GCAGCCAGTA	AAATCAAACA	GTTGGATCAG

5
10
15
20
25

```

1051 CACTACATAG TCCACAAGAT TGCCCATGCC ATAGCGGGCT GTGCGGCAGC
1101 GCGGCGGAAT AAGGGCAAGT GTCAGGATGG TCGGATAGGT GCGGCTGTGG
1151 GCGAGATAGT CGGGGAGGCT TTGACAAACG GCAAAAATCC TGACACTTTG
1201 ACAGCTAAAG AACGCGAACA GATTTTGGCA TACAGCAAAC TGGTTGCCGG
1251 TACGGTAAGC GGTGTGGTCG GCGGCGATGT AAATGCGGCG GCGAATGCGG
1301 CTGAGGTAGC GGTGAAAAAT AATCAGCTTA GCGACNAAGA GGGTAGAGAA
1351 TTTGATAACG AAATGACTGC ATGCGCCAAA CAGAATANTC CTCAACTGTG
1401 CAGAAAAAAT ACTGTAAAAA AGTATCAAAA TGTGCTGAT AAAAGACTTG
1451 CTGCTTCGAT TGCAATATGT ACGGATATAT CCGTAGTAC TGAATGTAGA
1501 ACAATCAGAA AACACATTT GATCGATAGT AGAAGCCTTC ATTCATCTTG
1551 GGAAGCAGGT CTAATTGGTA AAGATGATGA ATGGTATAAA TTATTCAGCA
1601 AATCTTACAC CCAAGCAGAT TTGGCTTTAC AGTCTTATCA TTTGAATACT
1651 GCTGCTAAAT CTGGCTTCA ATCGGGCAAT ACAAAGCCTT TATCCGAATG
1701 GATGTCCGAC CAAGTTTATA CACTTATTTT AGGAGTTAAT CCTAGATTCA
1751 TTCCAATACC AAGAGGGTTT GTAAAACAAA ATACACCTAT TACTAATGTC
1801 AAATACCCGG AAGGCATCAG TTTCGATACA AACCTANAAA GACATCTGGC
1851 AAATGCTGAT GGTTTTAGTC AAGAACAGGG CATTAAGGA GCCCATAACC
1901 GCACCAATNT TATGGCAGAA CTAATTCAC GAGGAGGANG NGTAAATCT
1951 GAAACCCANA CTGATATTGA AGGCATTACC CGAATTAAAT ATGAGATTCC
2001 TACACTAGAC AGGCAGGTA AACCTGATGG TGGATTAAAG GAAATTTCAA
2051 GTATAAAAC TGTTTATAAT CCTAAAAANT TTNNGATGA TAAATACTT
2101 CAAATGGCTC AANATGCTGN TTCACAAGGA TATTCAAAAG CCTCTAAAT
2151 TGCTCAAAAT GAAAGAACTA AATCAATATC GGAAAGAAAA AATGTCATTC
2201 AATTCTCAGA AACCTTGAC GGAATCAAAT TTAGANNNTA TNTNGATGTA
2251 AATACAGGAA GAATTACAAA CATTCACCCA GAATAATTTA A

```

This encodes a protein having amino acid sequence <SEQ ID 22>:

30
35
40

```

1 XQLLAEEGIH KHELDVQKSR RFIGIKVGXS NYSKNELNET KLPVRVVAQX
51 AATRSGWDTV LEGTEFKTTL AGADIQAGVX EKARVDKII LKGIVNRIQS
101 EEKLETNSTV WQKQAGRST IETLKLPSFE SPTPPKLSAP GGYIVDIPKG
151 NLKTEIEKLS KQPEYAYLKQ LQVAKNINWN QVQLAYDRWD YKQEGLTEAG
201 AAIIALAVTV VTSGAGTGAV LGLNGAXAAA TDAAAFASLAS QASVSFINNK
251 GDVGKTLKEL GRSSTVKNLV VAAATAGVAD KIGASALXNV SDKQWINNLT
301 VNLANAGSAA LINTAVNGGS LKDXLEANIL AALVNTAHGE AASKIKQLDQ
351 HYIVHKIAHA IAGCAAAAAN KGKQDGAIG AAVGEIVGEA LTNGKNPDTL
401 TAKEREQILA YSKLVAGTVS GVVGGDVNAA ANAAEVAVKN NQLSDXEGRE
451 FDNEMTACAK QNXPLCRKN TVKKYQNVAD KRLAASIAIC TDISRSTECR
501 TIRKQHLIDS RSLHSSWEAG LIGKDDEWYK LFSKSYTQAD LALQSYHLNT
551 AAKSWLQSGN TKPLSEWMSD QGYTLISGVN PRFIPIPRGF VKQNTPIITNV
601 KYPEGISFDT NLXRHLANAD GFSQEQGIK AHNRTNXMAE LNSRGGXVKS
651 ETXTDIEGIT RIKYEIPTLD RTGKPDGGFK EISSIKTVYN PKXFXDDKIL
701 QMAQXAXSQG YSKASKIAQN ERTKSISERK NVIQFSETFD GIKFRXYXDV
751 NTGRITNIHP E*

```

Based on the presence of a putative transmembrane domain, it is predicted that these proteins from *N.meningitidis*, and their epitopes, could be useful antigens for vaccines or diagnostics.

45 Example 5

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 23>

50

```

1 ..CGGATCGTTG TAGGTTTTCG GATTTCTTGC GCCGTAGTCA CCGTAGTCCC
51 AAGTATAACC CAAGGCTTTG TCTTCGCCTT TCATTCCGAT AAGGGATATG
101 ACGCTTTGGT CCGTATAGCC GTCTTGGGAA CCTTTGTCCA CCCAACGCAT
151 ATCTGCCTGC GGATTCTCAT TGCCGCTTCT TGGCTGCTGA TTTTCTGCC
201 TTCGCGTTTT TCAACTTCGC GCTTGAGGGC TTCGGCATAT TTGTCGGCCA
251 ACCCATTTC TTTCGGATGC AGCTGCCTAT TGTTCCAATC TACATTGCGA
301 CCCACCACAG CACCACCACT ACCACCAGTT GCATAG

```

This corresponds to the amino acid sequence <SEQ ID 24; ORF50>:

55

```

1 ..RIVVGLRISC AVVTVPVSIT QGFVFAFHSD KGYDALVGIA VLGTFFVHPTH
51 ICLRILIAAS WLLIFLPSRF STSRLRASAY LSANAISFGC SCLLFQSTFA
101 PTTAPPLPV A*

```

Computer analysis predicts two transmembrane domains and also indicates that ORF50 has no significant amino acid homology with known proteins.

Based on the presence of a putative transmembrane domain, it is predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

5 Example 6

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 25>

```

1  ..AAGTTTGA CT TTACCTGGTT TATTCCGGCG GTAATCAAAT ACCGCCGGTT
51  GTTTTTTGAA GTATTGGTGG TGTCGGTGGT GTTGCAGCTG TTTGCGCTGA
101 TTACGCCTCT GTTTTCCAA GTGGTGATGG ACAAGGTGCT GGTACATCGG
151 GGATTCTCTA CTTTGGATGT GGTGTCGGTG GCTTTGTTGG TGGTGTGCGT
201 GTTTGAGATT GTGTTGGGCG GTTGCGGAC GTATCTGTTT GCACATACGA
251 CTTCACGTAT TGATGTGGAA TTGGGCGCGC GTTTGTTCCG GCATCTGCTT
301 TCCCTGCCTT TATCCTATTT CGAGCACAGA CGAGTGGGTG ATACGGTGGC
351 TCGGGTGCGG GAATTGGAGC AGATTCGCAA TTTCTTGACC GGTGAGCGC
15  401 TGACTTCGGT GTTGGATTTG GCGTTTTCGT TTATCTTTCT GCGGGTGATG
451 TGGTATTACA GCTCCACTCT GACTTGGGTG GTATTGGCTT CGTTG.....
//
1451 .....
1501 ..... ..ATTGCGC
20  1551 CAACCGGACG GTGCTGATTA TCGCCACCG TCTGTCCACT GTTAAACGG
1601 CACACCGGAT CATTGCCATG GATAAAGGCA GGATTGTGGA AGCGGGAACA
1651 CAGCAGGAAT TGCTGGCGAA CG..AACGGA TATTACCGCT ATCTGTATGA
1701 TTTACAGAAC GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 26; ORF39>:

```

25  1  ..KFDFTWFIPA VIKYRRLLFFE VLVVSVVLQL FALITPLFFQ VVMDKVLVHR
51  GFSTLDVVSV ALLVVSLEFI VLGGLRITYLF AHTTSRIDVE LGARLFRHLL
101 SLPLSYFEHR RVGDTVARVR ELEQIRNFLT GQALTSVLDL AFSFIFLAVM
151 WYYSSTLTWV VLASL.....
//
30  501 ..... ICAVRT VLIHRLST VKTAHRIAM DKGRIVEAGT
551 QQELLANXNG YYRYLYDLQN G*

```

Further work revealed the complete nucleotide sequence <SEQ ID 27>:

```

35  1  ATGTCTATCG TATCCGCACC GCTCCCCGCC CTTTCCGCC TCATCATCCT
51  CGCCCATTA CACGGCATTG CCGCCAATCC TGCCGATATA CAGCATGAAT
101 TTTGTACTTC CGCACAGAGC GATTAAATG AAACGCAATG GCTGTTAGCC
151 GCCAAATCTT TGGGATTGAA GGCAAAGGTA GTCCGCCAGC CTATTAAACG
201 TTTGGCTATG GCGACTTTAC CCGCATTGGT ATGGTGTGAT GACGGCAACC
251 ATTTCAATTT GGCCAAAACA GACGGTGAGG GTGAGCATGC CCAATTTTG
301 ATACAGGATT TGGTTACGAA TAAGTCTGCG GTATTGTCTT TTGCCGAATT
40  351 TTCTAACAGA TATTCGGGCA AACTGATATT GGTGCTTCC CGCGCTTCGG
401 TATTGGGCG TTTGGCAAAG TTTGACTTTA CCTGGTTTAT TCCGGCGGTA
451 ATCAAATACC GCCGGTTGTT TTTTGAAGTA TTGGTGGTGT CGGTGGTGT
501 GCAGCTGTTT GCGCTGATTA CGCCTCTGTT TTTCCAAGTG GTGATGGACA
551 AGGTGCTGGT ACATCGGGGA TTCTCTACTT TGGATGTGGT GTCGGTGGCT
45  601 TTGTTGGTGG TGTCGCTGTT TGAGATTGTG TTGGGCGGTT TGCGGACGTA
651 TCTGTTTGCA CATACGACTT CACGTATTGA TGTGGAATTG GGCGCGCGTT
701 TGTTCCGGCA TCTGCTTTCC CTGCTTTTAT CCTATTTTCA GCACAGACGA
751 GTGGGTGATA CGGTGGCTCG GGTGCGGGAA TTGGAGCAGA TTCGCAATTT
801 CTTGACCGGT CAGCGCTGA CTTGCTGTTT GGATTGCGC TTTTCGTTTA
50  851 TCTTTCTGGC GGTGATGTGG TATTACAGCT CCACTCTGAC TTGGGTGGTA
901 TTGGCTTCGT TGCCTGCCTA TGCGTTTGG TCGGCATTTA TCAGTCCGAT
951 ACTGCGGACG CGTCTGAACG ATAAGTTCGC GCGCAATGCA GACAACCACT
1001 CGTTTTTAGT AGAAAGCATC ACTGCGGTGG GTACGGTAAA GGCGATGGCG
1051 GTGGAGCCGC AGATGACGCA CGCTTGGGAC AATCAGTTGG CGGCTTATGT

```


5	1101	GGCTTCGGGA	TTTCGGGTAA	CGAAGTTGGC	GGTGGTCGGC	CAGCAGGGGG
	1151	TGCAGCTGAT	TCAGAAGCTG	GTGACGGTGG	CGACGTTGTG	GATTGGCGCA
	1201	CGGCTGGTAA	TTGAGAGCAA	GCTGACGGTG	GGGCAGCTGA	TTGCGTTTAA
	1251	TATGCTCTCG	GGACAGGTGG	CGGCGCCTGT	TATCCGTTTG	GCGCAGTTGT
	1301	GGCAGGATT	CCAGCAGGTG	GGGATTTCGG	TGGCGGTTTG	GGGGGATATT
10	1351	CTGAATGCGC	CGACCGAGAA	TGCGTCTTCG	CATTTTGGCTT	TGCCGATAT
	1401	CCGGGGGGAG	ATTACGTTTC	AACATGTCGA	TTTCCGCTAT	AAGGCGGACG
	1451	GCAGGCTGAT	TTTGCAGGAT	TTGAACCTGC	GGATTTCGGGC	GGGGGAAGTG
	1501	CTGGGGATTG	TGGGACGTTT	GGGGTCGGGC	AAATCCACAC	TCACCAAATT
	1551	GGTGCCAGCT	CTGTATGTAC	CGGAGCAGGG	ACGGGTGTTG	GTGGACGGCA
15	1601	ACGATTTGGC	TTTGCCCGCT	CCTGCCTGGC	TGCGGC GGCA	GGTCGGCGTG
	1651	GTCTTGCAGG	AGAATGTGCT	GCTCAACCGC	AGCATACGCG	ACAATATCGC
	1701	GCTGACGGAT	ACGGGTATGC	CGCTGGAACG	CATTATCGAA	GCAGCCAAAC
	1751	TGGCGGGCGC	ACACGAGTTT	ATTATGGAGC	TGCCGGAAGG	CTACGGCACC
	1801	GTGGTGGCG	AACAAGGGGC	CGGCTTGTCG	GGCGGACAGC	GGCAGCGTAT
20	1851	TGCGATTGCC	CGCGCGTTAA	TCACCAATCC	GCGCATTCTG	ATTTTTGATG
	1901	AAGCCACCAG	CGCGCTGGAT	TATGAAAGTG	AACGAGCGAT	TATGCAGAAC
	1951	ATGCAGGCCA	TTTGCGCCAA	CCGACGGTGG	CTGATTATCG	CCCACCGTCT
	2001	GTCCACTGTT	AAAACGGCAC	ACCGGATCAT	TGCCATGGAT	AAAGGCAGGA
	2051	TTGTGGAAGT	GGGAACACAG	CAGGAATTGC	TGCCGAAGCC	GAACGGATAT
	2101	TACCGCTATC	TGTATGATTT	ACAGAACGGG	TAG	

This corresponds to the amino acid sequence <SEQ ID 28; ORF39-1>:

	1	MSIVSAPLPA	LSALIILAHY	HGIAANPADI	QHEFCTSAQS	DLNETQWLLA
25	51	AKSLGLKAKV	VRQPIKRLAM	ATLPALVWCD	DGNHFILAKT	DGEGEHAQFL
	101	IDQLVTNKSA	VLSFAEFSNR	YSGKLILVAS	RASVLGSLAK	FDFTWFIPAV
	151	IKYRRLFFEV	LVVSUVLQLF	ALITPLFFQV	VMDKVLVHRG	FSTLDVVSVA
	201	LLVVSLEFIV	LGLRLTYLFA	HTTSRIDVEL	GARLFRHLLS	LPLSYFEHRR
	251	VGDTVARVRE	LEQIRNFLTG	QALTSVLDLA	FSFIFLAVMW	YYSSTLTWVV
30	301	LASLPAYAFW	SAFISPIIRT	RLNDKFARNA	DNQSFLVESI	TAVGTVKAMA
	351	VEPQMTQRWD	NQLAAYVASG	FRVTKLAVVG	QQGVQLIQKL	VTVATLWIGA
	401	RLVIESKLTV	QGLIAFNMLS	GQVAAPVIRL	AQLWQDFQQV	GISVARLGDI
	451	LNAPTENASS	HLALPDIRGE	ITFEHVDFRY	KADGRILIQD	LNLRIRAGEV
	501	LGIVGRSGSG	KSTLTCLKVR	LYVPEQGRVL	VDGNDLALAA	PAWLRRQVGV
35	551	VLQENVLLNR	SIRDNIATLD	TGMPLERIIE	AAKLAGAHEF	IMELPEGYGT
	601	VVGEQGAGLS	GGQRQRIATA	RALITNPRIL	IFDEATSALD	YESERAIMQN
	651	MQAICANRTV	LIIAHLRSTV	KTAHRIIAMD	KGRIVEAGTQ	QELLAKPNGY
	701	YRYLYDLQNG	*			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.meningitidis* (strain A)

40 ORF39 shows 100% identity over a 165aa overlap with an ORF (ORF39a) from strain A of *N. meningitidis*:

```

                                     10      20      30
orf39.pep                           KEDFTWFIPAVIKYRRLFFEVLVVSVVLQL
                                         |||
45 orf39a          AVLSFAEFSNRYSGKLILVASRASVLGSLAKFEDFTWFIPAVIKYRRLFFEVLVVSVVLQL
                               110        120        130        140        150        160

                                     40      50      60      70      80      90
orf39.pep           FALITPLFFQVVMDKVLVHRGFSTLDVVSVALLLVSLFEIVLGGRLTYLFAHTTSRIDVE
                               |||
50 orf39a           FALITPLFFQVVMDKVLVHRGFSTLDVVSVALLLVSLFEIVLGGRLTYLFAHTTSRIDVE
                               170        180        190        200        210        220

                                     100      110      120      130      140      150
orf39.pep           LGARLFRHLLSLPLSYFEHRRVGDTVARVRELEQIRNFLTGQALTSVLDLAFSFIFLAVM
                               |||
55 orf39a           LGARLFRHLLSLPLSYFEHRRVGDTVARVRELEQIRNFLTGQALTSVLDLAFSFIFLAVM
                               230        240        250        260        270        280

                                     160      170      180      190      200      210
60 orf39.pep         WYYSSLTWVVLASLXXXXXXXXXXXXXXXXXXXXXICANRTVLIIAHRLSTV

```

orf39a |||||
 WYYSSTLTWVVLASLPAYAFWSAFISPILRTRLNDKFARNADNQSFLVESITAVGTVKAM
 290 300 310 320 330 340

ORF39-1 and ORF39a show 99.4% identity in 710 aa overlap:

5	orf39-1.pep	MSIVSAPLPALSALIILAHYHGIAANPADIQHEFCTSAQSDLNQWLLAAKSLGLKAKV
	orf39a	MSIVSAPLPALSALIILAHYHGIAANPADIQHEFCTSAQSDLNQWLLAAKSLGLKAKV
10	orf39-1.pep	VRQPIKRLAMATLPALVWCDDGNHFILAKTDGEGEHAQFLIQDLVTNKSAVLSFAEFSNR
	orf39a	VRQPIKRLAMATLPALVWCDDGNHFILAKTDGGGEHAQYLIQDLTTNKSAVLSFAEFSNR
15	orf39-1.pep	YSGKLILVASRASVLGSLAKFDTWFIPAVIKYRRLFFEVLVSVVLQLFALITPLFFQV
	orf39a	YSGKLILVASRASVLGSLAKFDTWFIPAVIKYRRLFFEVLVSVVLQLFALITPLFFQV
20	orf39-1.pep	VMDKVLVHRGFSTLDVVSVALLVSLFEIVLGGLRITYLFAHTTSRIDVELGARLFRHLLS
	orf39a	VMDKVLVHRGFSTLDVVSVALLVSLFEIVLGGLRITYLFAHTTSRIDVELGARLFRHLLS
25	orf39-1.pep	LPLSYFEHRRVGD TVARVRELEQIRNFLTGOALTSVLDLAFSFI FLAVMWYYSSTLTWVV
	orf39a	LPLSYFEHRRVGD TVARVRELEQIRNFLTGOALTSVLDLAFSFI FLAVMWYYSSTLTWVV
30	orf39-1.pep	LASLPAYAFWSAFISPILRTRLNDKFARNADNQSFLVESITAVGTVKAMAVEPQMTQRWD
	orf39a	LASLPAYAFWSAFISPILRTRLNDKFARNADNQSFLVESITAVGTVKAMAVEPQMTQRWD
35	orf39-1.pep	NQLAAYVASGFRVTKLAVVGQGVQLIQKLVTVATLWIGARLVIESKLTVGQLIAFNMLS
	orf39a	NQLAAYVASGFRVTKLAVVGQGVQLIQKLVTVATLWIGARLVIESKLTVGQLIAFNMLS
40	orf39-1.pep	GQVAAPVIRLAQLWQDFQQVGISVARLGDILNAPTENASSHLALPDIRGEITFEHVDFRY
	orf39a	GQVAAPVIRLAQLWQDFQQVGISVARLGDILNAPTENASSHLALPDIRGEITFEHVDFRY
45	orf39-1.pep	KADGRILQLDLNLRIRAGEVLGIVGRSGSGKSTLTKLVQRLYPVPEQGRVLVDGNDLALAA
	orf39a	KADGRILQLDLNLRIRAGEVLGIVGRSGSGKSTLTKLVQRLYPVPAQGRVLVDGNDLALAA
50	orf39-1.pep	PAWLRRQGVVVLQENVLLNRSIRDNIALTDTGMPLERIEAAKLAGAHEFIMELPEGYGT
	orf39a	PAWLRRQGVVVLQENVLLNRSIRDNIALTDTGMPLERIEAAKLAGAHEFIMELPEGYGT
55	orf39-1.pep	VVGEQGAGLSGGQRQRIARALITNPRILIFDEATSALDYESERAIMQNMQAICANRTV
	orf39a	VVGEQGAGLSGGQRQRIARALITNPRILIFDEATSALDYESERAIMQNMQAICANRTV
60	orf39-1.pep	LIIAHLSTVKTAHRIIAMDKGRIVEAGTQQELLAKPNGYRYLYDLQNGX
	orf39a	LIIAHLSTVKTAHRIIAMDKGRIVEAGTQQELLAKPNGYRYLYDLQNGX

The complete length ORF39a nucleotide sequence <SEQ ID 29> is:

	1	ATGTCTATCG	TATCCGCACC	GCTCCCCGCC	CTTTCGCCCC	TCATCATCCT
55	51	CGCCCATAC	CACGGCATTG	CCGCCAATCC	TGCCGATATA	CAGCATGAAT
	101	TTTGTAATC	CGCACAGAGC	GATTTAAATG	AAACGCAATG	GCTGTTAGCC
	151	GCCAAATCTT	TGGGATTGAA	GGCAAAGGTA	GTCCGCCAGC	CTATTAACG
	201	TTTGGCTATG	GCGACTTTAC	CCGCATTGGT	ATGGTGTGAT	GACGGCAACC
	251	ATTTTATTTT	GGCTAAAACA	GACGGTGGGG	GTGAGCATGC	CCAATATCTA
60	301	ATACAGGATT	TAACACGAA	TAAGCTGCG	GTATTGTCTT	TTGCCGAATT
	351	TTCTAACAGA	TATTCGGGCA	AACTGATATT	GGTTGCTTCC	CGCGCTTCGG
	401	TATTGGGCAG	TTTGGCAAAG	TTTGACTTTA	CCTGGTTTAT	TCCGGCGGTA
	451	ATCAAATACC	GCCGGTTGTT	TTTGAAGTA	TTGGTGGTGT	CGGTGGTGTT
	501	GCAGCTGTTT	GCGCTGATTA	CGCCTCTGTT	TTTCCAAGTG	GTGATGGACA
65	551	AGGTGCTGGT	ACATCGGGGA	TTCTCTACTT	TGGATGTGGT	GTGGTGGCT
	601	TTGTTGGTGG	TGTCGCTGTT	TGAGATTGTG	TTGGGCGGTT	TGCGGACGTA
	651	TCTGTTTGCA	CATACGACTT	CACGTATTGA	TGTGGAATTG	GGCGCGCGTT

701 TGTTCGGGCA TCTGCTTTCC CTGCCTTTAT CCTATTTCTGA GCACAGACGA
 751 GTGGGTGATA CGGTGGCTCG GGTGCGGGAA TTGGAGCAGA TTCGCAATTT
 801 CTTGACCGGT CAGGCGCTGA CTTCCGGTGT GGATTTGGCG TTTTCGTTTA
 851 TCTTTCTGGC GGTGATGTGG TATTACAGCT CCACTCTGAC TTGGGTGGTA
 901 TTGGCTTCGT TGCCTGCCTA TCGGCTTTGG TCGGCATTTA TCAGTCCGAT
 951 ACTGCGGACG CGTCTGAACG ATAAGTTCGC GCGCAATGCA GACAACCACT
 1001 CGTTTTTAGT AGAAAGCATC ACTGCGGTGG GTACGGTAAA GGCGATGGCG
 1051 GTGGAGCCGC AGATGACGCA GCGTTGGGAC AATCAGTTGG CGGCTTATGT
 1101 GGCTTCGGGA TTTCGGGTAA CGAAGTTGGC GGTGGTCGGC CAGCAGGGGG
 1151 TGCAGCTGAT TCAGAAGCTG GTGACGGTGG CGACGTTGTG GATTGGCGCA
 1201 CGGCTGGTAA TTGAGACCAA GCTGACGGTG GGGCAGCTGA TTGCGTTTAA
 1251 TATGCTCTCG GGACAGGTGG CGGCGCCTGT TATCCGTTTG GCGCAGTTGT
 1301 GGCAGGATTT CCAGCAGGTG GGGATTTTCGG TGGCGCGTTT GGGGGATATT
 1351 CTGAATGCGC CGACCGAGAA TCGCTCTTCG CATTGGGCTT TGCCCCGATAT
 1401 CCGGGGGGAG ATTACGTTCC AACATGTCGA TTTCCGCTAT AAGGCGGACG
 1451 GCAGGCTGAT TTTGCAGGAT TTGAACCTGC GGATTCGGGC GGGGGAAGTG
 1501 CTGGGGATTG TGGGACGTTT GGGGTCGGGC AAATCCACAC TCACCAAATT
 1551 GGTGCAGCGT CTGTATGTAC CGGCGCAGGG ACGGGTGTG GTGGACGGCA
 1601 ACGATTTGGC TTTGGCCGCT CCTGCTTGGC TCGGCGGGCA GGTCCGCGTG
 1651 GTCTTGACAG AGAATGTGCT GCTCAACCGC AGCATACGCG ACAATATCGC
 1701 GCTGACGGAT ACGGGTATGC CGCTGGAACG CATTATCGAA GCAGCCAAAC
 1751 TGGCGGGCGC ACACGAGTTT ATTATGGAGC TGCCGGAAGG CTACGGCACC
 1801 GTGGTGGGCG AACAAGGGGC CGGCTGTGCG GCGGACAGC GGCAGCGTAT
 1851 TGCGATTGCC CGCGCGTTAA TCACCAATCC GCGCATTCTG ATTTTGTATG
 1901 AAGCCACCAG CGCGCTGGAT TATGAAAGTG AACGAGCGAT TATGCAGAAC
 1951 ATGCAGGCCA TTTGCGCCAA CCGGACGGTG CTGATTATCG CCCACCGTCT
 2001 GTCCACTGTT AAAACGGCAC ACCGGATCAT TGCCATGGAT AAAGCAGGA
 2051 TTGTGGAAGC GGGAACACAG CAGGAATTGC TGGCGAAGCC GAACGGATAT
 2101 TACCGCTATC TGTATGATT ACAGAACGGG TAG

30 This encodes a protein having amino acid sequence <SEQ ID 30>:

1 MSIVSAPLPA LSALIILAHY HGIAANPADI QHEFCTSAQS DLNETQWLLA
 51 AKSLGLKAKV VRQPIKRLAM ATLPALVWCD DGNHFILAKT DGGGEHAQYL
 101 IQDLTTNKSA VLSFAEFSNR YSGKLILVAS RASVLGSLAK FDFTWFIPAV
 151 IKYRRLFFEV LVVSVVLQLE ALITPLFFQV VMDKVLVHRG FSTLDVVSVA
 201 LLVVSLEFIV LGGLRTRYLFA HTTSRIDVEL GARLFRHLLS LPLSYFEHRR
 251 VGDTVARVRE LEQIRNFLTG QALTSVLDLA FSFIFLAVMW YYSSTLTWV
 301 LASLPAYAFW SAFISPIRRT RLNDKFARNA DNQSFLVESI TAVGTVKAMA
 351 VEPQMTQRWD NQLAAYVASG FRVTKLAVVG QQGVQLIQLK VTVATLWIGA
 401 RLVIKSLTV GQLIAFNMLS GQVAAPVIRL AQLWQDFQV GISVARLGDI
 451 LNAPTENASS HLAALPDIRGE ITFEHVDFRY KADGRLLIQD LNLIRIRAGEV
 501 LGIVGRSGSG KSTLTKLVR LYVPAQGRVL VDGNDLALAA PAWLRRQVGV
 551 VLQENVLLNR SIRDNIATLD TGMPLERIIE AAKLAGAHEF IMELPEGYGT
 601 VVGEQAGLS GGQRQRIIA RALITNPRIL IFDEATSALD YESERAIMQN
 651 MQAICANRTV LIIAHLSTV KTAHRIIAMD KGRIVEAGTQ QELLAKPNGY
 701 YRYLYDLQNG *

ORF39a is homologous to a cytolysin from *A. pleuropneumoniae*:

sp|P26760|RT1B_ACTPL RTX-I TOXIN DETERMINANT B (TOXIN RTX-I SECRETION ATP-
 BINDING PROTEIN) (APX-IB) (HLY-IB) (CYTOLYSIN IB) (CLY-IB)
 >gi|97137|pir||D43599 cytolysin IB - Actinobacillus pleuropneumoniae (serotype 9)
 50 >gi|38944 (X61112) ClyI-B protein [Actinobacillus pleuropneumoniae] Length = 707
 Score = 931 bits (2379), Expect = 0.0
 Identities = 472/690 (68%), Positives = 540/690 (77%), Gaps = 3/690 (0%)
 Query: 20 YHGIAANPADIQHEFCTSAQSDLNETQWXXXXXXXXXXXXVVRQPIKRLAMATLPALVWC 79
 YH IA NP +++H+F + -L+ T W V++ I RLA LPALVW
 55 Sbjct: 20 YHNIADVNPPEELKHKFDLEGKG-LDLTAWLLAAKSLELKAKQVKKAIIDRLAFIALPALVWR 78
 Query: 80 DDGNHFILAKTDGGGEHAQYLIQDLTTNKSAVLSFAEFSNRYSGKLILVASRASVLGSLA 139
 +DG HFIL K D E +YLI DL T+ +L AEF + Y GKLILVASRAS++G LA
 60 Sbjct: 79 EDGKHFILTKIDN--EAKKYLIFFDLETHNPRILEQAEFESLYQGKLILVASRASIVGKLA 136
 Query: 140 KFDFTWFIPAVIKYRXXXXXXXXXXXXXXXXXITPLFFQVMDKVLVHRGFXXXXXXXXX 199
 KFDFTWFIPAVIKYR+ ITPLFFQVMDKVLVHRGF
 65 Sbjct: 137 KFDFTWFIPAVIKYRKIFETLIVSIFLQIFALITPLFFQVMDKVLVHRGFSTLNVITV 196
 Query: 200 XXXXXXXFEIVLGGLRTRYLFAHTTSRIDVELGARLFRHLLSLPLSYFEHRRVGDTVARVR 259

FEIVL GLRTY+FAH+TSRIDVELGARLFRHLL+LP+SYFE+RRVGD TVARVR
 Sbjct: 197 ALAIVVLFEIVLNGLR TYIFAHSTSRIDVELGARLFRHLLALPISYFENRRVGD TVARVR 256

5 Query: 260 ELEQIRNFLT GQALTSVLDLAFS FIFLAVM WYYSS TLTWVVLASLPAYAFWSAFISPILR 319
 EL+QIRNFLT GQALTSVLDL FSFIF AVMWYYS LT V+L SLP Y WS FISPI LR
 Sbjct: 257 ELDQIRNFLT GQALTSVLDL MFSFIFFAVMWYYS PKLTLVILGSLP FYMGWSIFISPILR 316

10 Query: 320 TRLN DKFARNADNQSF LVESITAVGT VKAMAVEPQMTQRWDNQLAAYVASGFRVTKLAVV 379
 RL++KFAR ADNQSFLVES+TA+ T+KA+AV PQMT WD QLA+YV++GFRVT LA +
 Sbjct: 317 RRLDEKFARGADNQSF LVESVTAINTIKALAVTPQMTNTWDKQLASYVSAGFRVTTLATI 376

15 Query: 380 GQQGVQLIQKLVTVATLWIGARLVIESKLT V GQLIAFNMLSGQVAAPVIRLAQLWQDFQQ 439
 GQQGVQ IQK+V V TLW+GA LVI L++GQLIAFNMLSGQV APVIRLAQLWQDFQQ
 Sbjct: 377 GQQGVQFIQKVVMVITLWLG AHLVISGDL SIGQLIAFNMLSGQVIAPVIRLAQLWQDFQQ 436

20 Query: 440 VGISVARLGDILNAPTENASSHLALPDIRGEITFEHVDFRYKADGR LILQDNLNLRIRAGE 499
 VGISV RLGD+LN+PTE+ LALP+I+G+ITF ++ FRYK D +IL D+NL I+ GE
 Sbjct: 437 VGISVTRLGDVLNSPTESYQ GKALALPEIKGDITFRNIRFRYKPDAPVILNDVNL SIQQGE 496

25 Query: 500 VLGIVGRSGSGKSTLT KLVRQRYVPAQGRVLVDGNDLALAPAWLRRQVGVLQENVLLN 559
 V+GIVGRSGSGKSTLT KL+QR Y+P G+VL+DG+DLALA P WLRRQVGVLQ+NVLLN
 Sbjct: 497 VIGIVGRSGSGKSTLT KLIRFYIPENGQVLIDGHD LALADPNWLRQVGVLQDNVLLN 556

30 Query: 560 RSIRDNIALTDTGMPLERIIEAAKLAGAHEFIMELPEGYGT VVGEQGAGLSGGQRQRIAI 619
 RSIRDNIAL D GMP+E+I+ AAKLAGAHEFI EL EGY T+VGEQGAGLSGGQRQRIAI
 Sbjct: 557 RSIRDNIALADPGMPMEKIVHAAKLAGAHEFISELREGYNTIVGEQGAGLSGGQRQRIAI 616

35 Query: 620 ARALITNPRILIFDEATSALDYESERAIMQNMQAICANRTVLIIAHRLSTVKT AHRIIAM 679
 ARAL+ NP+ILIFDEATSALDYESE IM+NM IC RTV+IIAHRLSTVK A RII M
 Sbjct: 617 ARALVNNPKILIFDEATSALDYESEHIIMRNMHQICKGRTVIIIAHRLSTVKNADRIIVM 676

Query: 680 DKGRIVEAGTQQELLAKPNGYRYLYDLQN 709
 +KG+IVE G +ELLA PNG Y YL+ LQ+
 Sbjct: 677 EKGQIVEQGHKELLADPNGLYHYLHQLQS 706

Homology with the HlyB leucotoxin secretion ATP-binding protein of *Haemophilus actinomycetemcomitans* (accession number X53955)

ORF39 and HlyB protein show 71% and 69% amino acid identity in 167 and 55 overlap at the N- and C-terminal regions, respectively:

40 Orf39 1 KFDFTWFIPAVIKYRXXXXXXXXXXXXXXXXXITPLFFQVMDKVLVHRGFXXXXXXXXX 60
 KFDFTWFIPAVIKYR+ ITPLFFQVMDKVLVHRGF
 HlyB 137 KFDFTWFIPAVIKYRKIFETLIVSIFLQIFALITPLFFQVMDKVLVHRGFSTLNVITV 196

45 Orf39 61 XXXXXXXFEIVLGGRLTYLFAHTTSRIDVELGARLFRHLLSLPLSYFEHRRVGD TVARVR 120
 FEI+LGGLRTY+FAH+TSRIDVELGARLFRHLL+LP+SYFE RRVGD TVARVR
 HlyB 197 ALAIVVLFEIILGGRLTYVFAHSTSRIDVELGARLFRHLLALPISYFEARRVGD TVARVR 256

50 Orf39 121 ELEQIRNFLT GQALTSVLDLAFS FIFLAVM WYYSS TLTWVVLASLIC 167
 EL+QIRNFLT GQALTS+LDL FSFIF AVMWYYS LT VVL SL C
 HlyB 257 ELDQIRNFLT GQALTSILDLLFSFIFFAVMWYYS PKLTLVVLGSLPC 303

//

55 Orf39 166 ICANRTVLIIAHRLSTVKT AHRIIAMDKGRIVEAGTQQELLANXNGYRYLYDLQ 220
 IC NRTVLIIAHRLSTVK A RII MDKG I+E G QELL + G Y YL+ LQ
 HlyB 651 ICNRTVLIIAHRLSTVKNADRIIVMDKGEIIEQGHQELLKDEKGLYSYLHQLQ 705

Based on this analysis, it is predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 7

60 The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 31>

```

1  ATGAAATACT TGATCCGCAC CGCCTTACTC GCAGTCGCAG CCGCCGGCAT
51 CTACGCCTGC CAACCGCAAT CCGAAGCCGC AGTGCAAGTC AAGGCTGAAA
101 ACAGCCTGAC CGCTATGCGC TTAGCCGTCG CCGACAAACA GGCAGAGATT
151 GACGGGTTGA ACGCCCAAk sGACGCCGAA ATCAGA...

```

5 This corresponds to the amino acid sequence <SEQ ID 32; ORF52>:

```

1  MKYLIRTALL AVAAAGIYAC QPOSEAAVQV KAENSLTAMR LAVADKQAEI
51 DGLNAQXDAE IR..

```

Further work revealed the complete nucleotide sequence <SEQ ID 33>:

```

10      1  ATGAAATACT TGATCCGCAC CGCCTTACTC GCAGTCGCAG CCGCCGGCAT
        51 CTACGCCTGC CAACCGCAAT CCGAAGCCGC AGTGCAAGTC AAGGCTGAAA
        101 ACAGCCTGAC CGCTATGCGC TTAGCCGTCG CCGACAAACA GGCAGAGATT
        151 GACGGGTTGA ACGCCCAAAT CGACGCCGAA ATCAGACAAC GCGAAGCCGA
        201 AGAATTGAAA GACTACCGAT GGATACACGG CGACGCCGAA GTGCCGGAGC
        251 TGGAAAAATG A

```

15 This corresponds to the amino acid sequence <SEQ ID 34; ORF52-1>:

```

1  MKYLIRTALL AVAAAGIYAC QPOSEAAVQV KAENSLTAMR LAVADKQAEI
51 DGLNAQIDAE IRQREAEELK DYRWIHGDAE VPELEK*

```

Computer analysis of this amino acid sequence predicts a prokaryotic membrane lipoprotein lipid attachment site (underlined).

20 ORF52-1 (7kDa) was cloned in the pGex vectors and expressed in *E.coli*, as described above. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification of the GST-fusion. Figure 4B shows plots of hydrophilicity, antigenic index, and AMPHI regions for ORF52-1.

Based on this analysis, it is predicted that this protein from *N.meningitidis*, and its epitopes, could
25 be useful antigens for vaccines or diagnostics.

Example 8

The following DNA sequence was identified in *N.meningitidis* <SEQ ID 35>

```

30      1  ATGGTTATCG GAATATTACT CGCATCAAGC AAGCATGCTC TTGTCATTAC
        51 TCTATTGTTA AATCCCCTCT TCCATGCATC CAGTTGCGTA TCGCGTtsGG
        101 CAATACGGAA TAAAAtCTGC TGTTCGCTT TGGCTAAATT TGCCAAATTG
        151 TTTATTGTTT CTTTAGGaGC AGCTTGCTTA GCCGCCTTCG CTTTCGACAA
        201 CGCCCCCACA GCGCCTTCCC AAGCgTTGCC TACCGTTACC GCACCCGTGG
        251 CGATTCCCGC GCCCGCTTCG GCAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 36; ORF56>:

```

35      1  MVIGILLASS KHALVITLLL NPVFHASSCV SRXAIRNKIC CSALAKFAKL
        51 FIVSLGAACL AAFAFDNAPT GASQALPTVT APVAIPAPAS AA*

```

Further work revealed the complete nucleotide sequence <SEQ ID 37>:

```

1  ATGGCTTGTA CAGGTTTGAT GGTTTTCCG TTAATGGTTA TCGGAATATT

```

51 ACTTGCATCA AGCAAGCCTG CTCCTTTCCT TACTCTATTG TTAAATCCCG
 101 TCTTCCATGC ATCCAGTTGC GTATCGCGTT GGGCAATACG GAATAAAATC
 151 TGCTGTTCTG CTTTGGCTAA ATTTGCCAAA TTGTTTATTG TTTCTTTAGG
 201 AGCAGCTTGC TTAGCCGCCT TCGCTTTCGA CAACGCCCCC ACAGGCGCTT
 251 CCCAAGCGTT GCCTACCGTT ACCGCACCCG TGGCGATTCC CGCGCCCGCT
 301 TCGGCAGCCT GA

This corresponds to the amino acid sequence <SEQ ID 38; ORF56-1>:

1 MACTGLMVFP LMVIGILLAS SKPAPFLTLL LNPVFHASSC VSRWAIRNKI
 51 CCSALAKFAK LFIVSLGAAC LAFAFDNAP TGASQALPTV TAPVAIPAPA
 101 SAA*

Computer analysis of this amino acid sequence predicts a leader peptide (underlined) and suggests that ORF56 might be a membrane or periplasmic protein.

Based on this analysis, it is predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

15 Example 9

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 39>

1 ATGTTCAAGTA TTTTAAATGT GTTCTTCAT TGTATTCTGG CTGTGTAGT
 51 CTCTGGTGAG ACGCCTACTA TATTTGGTAT CCTTGCTCTT TTTTACTTAT
 101 TGTATCTTTC TTATCTTGCT GTTTTAAAGA TTTTCTTTTC TTTTTCCTTA
 151 GACAGAGTTT CACTCCGGTC TCCCAGGCTG GAGTGCAAAT GGCATGACCC
 201 TTTGGCTCAC TGGCTCACGG CCACTTCTGC TATTCTGCCG CCTCAGCCTC
 251 CAGGG...

This corresponds to the amino acid sequence <SEQ ID 40; ORF63>:

1 MFSILNVFLH CILACVVSGE TPTIFGILAL FYLLYLSYLA VFKEIFFSFFL
 51 DRVSLRSPRL ECKWHDPLAH WLTATSAILP PQPPG...

Computer analysis of this amino acid sequence predicts a transmembrane region.

Based on this analysis, it is predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 10

30 The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 41>

1 ..GTGCGGACGT GGTGGTGTTC TTGGTTGCAG CGTTTGAAAT ACCCGTTGTT
 51 GCTTTGGATT GCGGATATGT TGCTGTACCG GTTGTGGGC GGCGCGGAAA
 101 TCGAATGCGG CCGTTGCCCT GTGCCGCCGA TGACGGATTG GCAGCATTTT
 151 TTGCCGCGCA TGGGAACGGT GTCGGCTTGG GTGGCGGTGA TTTGGGCATA
 201 CCTGATGATT GAAAGTGAAA AAAACGGAAG ATATTGA

This corresponds to the amino acid sequence <SEQ ID 42; ORF69>:

1 ..VRTWLVFVLQ RLKYPILLWI ADMLLYRLLG GAEIECGRCP VPPMTDWQHF
 51 LPAMGTVSAW VAVIWAYLMI ESEKNGRY*

Computer analysis of this amino acid sequence predicts a transmembrane region.

A corresponding ORF from strain A of *N.meningitidis* was also identified:

Homology with a predicted ORF from *N.meningitidis* (strain A)

ORF69 shows 96.2% identity over a 78aa overlap with an ORF (ORF69a) from strain A of *N.meningitidis*:

```

      10      20      30      40      50      60
orf69.pep  VRTWL VFWLQRLKYPLLW IADMLLYRLLGGAEIECGRCVPVPPMTDWQHFLPAMGTVSAW
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
orf69a     VRTWL VFWLQRLKYPLL LCIADMLLYRLLGGAEIECGRCVPVPPMTDWQHFLPTMGTVAAW
      10      20      30      40      50      60

      70      79
orf69.pep  VAVIWAYLMIESEKNGRYX
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
orf69a     VAVIWAYLMIESEKNGRYX
      70
  
```

The ORF69a nucleotide sequence <SEQ ID 43> is:

```

      1  GTGCGGACGT GGTGGTTTT TTGGTTGCAG CGTTTGAAAT ACCCGTTGTT
20  51  GCTTTGTATT GCGGATATGC TGCTGTACCG GTTGTGGGC GGCGCGGAAA
      101 TCGAATGCGG CCGTTGCCCT GTACCGCCGA TGACGGATTG GCAGCATTTT
      151 TTGCCGACGA TGGGAACGGT GGCGGCTTGG GTGGCGGTGA TTTGGGCATA
      201 CCTGATGATT GAAAGTGAAA AAAACGGAAG ATATTGA
  
```

This encodes a protein having amino acid sequence <SEQ ID 44>:

```

25  1  VRTWL VFWLQ RLKYPLL LCI ADMLLYRLLG GAEIECGRCP VPPMTDWQHF
      51  LPTMGTVAAW VAVIWAYLMI ESEKNGRY*
  
```

Based on this analysis, it is predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 11

30 The following DNA sequence was identified in *N.meningitidis* <SEQ ID 45>

```

      1  ATGTTTCAAA ATTTTGATTT GGGCGTGTTT CTGCTTGCCG TCCTCCCGCT
      51  GCTGCCCTCC ATTACCGTCT CGCACGTGGC GCGCGGCTAT ACGGCGCGCT
      101  ACTGGGGAGA CAACACTGCC GAACAATACG GCAGGCTGAC ACTGAACCCC
35  151  CTGCCCCATA TCGATTTGGT CGGCACAATC ATCgTACCGC TGCTTACTTT
      201  GATGTTACAG CCCTTCCTGT TCGGCTGGGC GCGTCCGATT CCTATCGATT
      251  CGCGCAACTT CCGCAACCCG cGCCTTGCTT GGCCTTGCGT TGCCGCGTCC
      301  GGCCCGCTGT CGAATCTAGC GATGGCTGTw CTGTGGGGCG TGGTTTGGT
      351  GCTGACTCCG TATGTCGGCG GGGCGTATCA GATGCCGTTG GCTCAAATGG
40  401  CAAACTACGG TATTCGTATC AATGCGATTC TGTTCCGCGT CAACATCATC
      451  CCCATCCTGC CTTGGGACGG CGGCATTTTC ATCGACACCT TCCTGTGCGG
      501  GAAATATTCG CAAGCGTTCC GCAAAATCGA ACCTTATGGG ACGTGGATTA
      551  TCCTACTGCT GATGCTGACC sGGGTTTGG GTGCGTTTAT wGCACCGATT
      601  sTGCgGmTgc GTGATTGCrT TTGTGCAGAT GTwCGTCTGA CTGGCTTTCA
      651  GACGGCATAA
  
```

45 This corresponds to the amino acid sequence <SEQ ID 46; ORF77>:

```

1 MFQNFDLGVF LLAVLPVLPS ITVSHVARGY TARYWGDNTA EQYGRLTINP
51 LPHIDLVGTI IVPLLTLMFT PFLFGWARPI PIDSRNFRNP RLAWRCVAAS
101 GPLSNLAMAV LWGVVLVLT YVGGAYQMPL AQMANYGILI NAILFALNII
151 PILPWDGGIF IDTFLSAKYS QAFRKIEPYG TWIILLMLT XVLGAFIAP
201 XRXRDCXCAD VRLTGFQTA*

```

Further work revealed the complete nucleotide sequence <SEQ ID 47>:

```

1 ATGTTTCAAA ATTTTGATTT GGGCGTGTTT CTGCTTGCCG TCCTGCCCGT
51 GCTGCTCTCC ATTACCGTCA GGGAGGTGGC GCGCGGCTAT ACGGCGCGCT
101 ACTGGGGAGA CAACACTGCC GAACAATACG GCAGGCTGAC ACTGAACCCC
151 CTGCCCCATA TCGATTGGT CCGCACAAATC ATCGTACCGC TGCTTACTTT
201 GATGTTACAG CCCTTCCTGT TCGGCTGGGC GCGTCCGATT CCTATCGATT
251 CGCGCAACTT CCGCAACCG CCGCTTGCTT GCGGTGCGT TGCCGCGTCC
301 GGCCCGCTGT CGAATCTAGC GATGGCTGTT CTGTGGGGCG TGGTTTGGT
351 GCTGACTCCG TATGTCGGCG GGGCGTATCA GATGCCGTTG GCTCAAATGG
401 CAAACTACGG TATTCTGATC AATGCGATTC TGTCGCGCT CAACATCATC
451 CCCATCCTGC CTTGGGACGG CGGCATTTTC ATCGACACCT TCCTGTCGGC
501 GAAATATTCG CAAGCGTTC GCAAAATCGA ACCTTATGGG ACGTGGATTA
551 TCCTACTGCT GATGCTGACC GGGGTTTGG GTGCGTTTAT TGCACCGATT
601 GTGCGGCTGG TGATTGCGTT TGTGCAGATG TTCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 48; ORF77-1>:

```

1 MFQNFDLGVF LLAVLPVLLS ITVREVARGY TARYWGDNTA EQYGRLTINP
51 LPHIDLVGTI IVPLLTLMFT PFLFGWARPI PIDSRNFRNP RLAWRCVAAS
101 GPLSNLAMAV LWGVVLVLT YVGGAYQMPL AQMANYGILI NAILFALNII
151 PILPWDGGIF IDTFLSAKYS QAFRKIEPYG TWIILLMLT GVLGAFIAP
201 VRLVIAFVQM FV*

```

Computer analysis of this amino acid sequence reveals a putative leader sequence and several transmembrane domains.

A corresponding ORF from strain A of *N.meningitidis* was also identified:

Homology with a predicted ORF from *N.meningitidis* (strain A)

ORF77 shows 96.5% identity over a 173aa overlap with an ORF (ORF77a) from strain A of *N.meningitidis*:

```

10      20      30      40      50      60
orf77.pep MFQNFDLGVFLLAVLPVLPSITVSHVARGYTARYWGDNTAEQYGRLTINPLPHIDLVGTI
35 orf77a          RGYTARYWGDNTAEQYGRLTINPLPHIDLVGTI
                        10      20      30

70      80      90      100     110     120
orf77.pep IVPLLTLMFTFPFLFGWARPIPIDSRNFRNPRLAWRCVAASGPLSNLAMAVLWGVVLVLT
40 orf77a IVPLLTLMFTFPFLFGWARPIPIDSRNFRNPRLAWRCVAASGPLSNLAMAVLWGVVLVLT
                        40      50      60      70      80      90

130     140     150     160     170     180
orf77.pep YVGGAYQMPLAQMANYGILINAILFALNIIIPILPWDGGIFIDTFLSAKYSQAFRKIEPYG
45 orf77a YVGGAYQMPLAQMANYXILINAILXALNIIIPILPWDGGIFIDTFLSAKXSQAFRKIEPYG
                        100     110     120     130     140     150

190     200     210     220
orf77.pep TWIILLMLTXVLGAFIAPIXRXRDCXCADVRLTGFQTA
50 orf77a TWIIXLLMLTGVLGAXIAPIVQLVIAFVQMFVX
                        160     170     180

```


ORF77-1 and ORF77a show 96.8% identity in 185 aa overlap:

		10	20	30	40	50	60
5	orf77-1.pep	MFQNFDLGVFLLAVLPVLLSITVREVARGYTARYWGDNTAEQYGRLT	LNPLPHIDLVTI				
	orf77a			RGYTARYWGDNTAEQYGRLT	LNPLPHIDLVTI		
				10	20	30	
10	orf77-1.pep	70	80	90	100	110	120
	orf77a	IVP	LLTLMFTPF	LEFGWARPI	PIDSRNFRN	PRLAWRCVA	ASGPLSNLAMAVLWGVVLVLT
		40	50	60	70	80	90
15	orf77-1.pep	130	140	150	160	170	180
	orf77a	YVGGAYQMPLAQ	MANYGILINAILFALNII	PILPWDGGIFIDTFLSAKYSQAF	RKIEPYG		
		100	110	120	130	140	150
20	orf77-1.pep	190	200	210			
	orf77a	TWII	LLMLTGVLGAFI	APIVRLVIAFVQMFVX			
25		160	170	180			

A partial ORF77a nucleotide sequence <SEQ ID 49> was identified:

	1	..CGCGGCTATA	CAGCGCGCTA	CTGGGGTGAC	AACACTGCCG	AACAATACGG
	51	CAGGCTGACA	CTGAACCCCC	TGCCCCATAT	CGATTTGGTC	GGCACAATCA
30	101	TCGTACCGCT	GCTTACTTTG	ATGTTTACGC	CCTTCTGT	CGGCTGGGCG
	151	CGTCCGATTC	CTATCGATTC	GCGCAACTTC	CGCAACCCGC	GCCTTGCCTG
	201	GCGTTCGCTT	GCCGCGTCCG	GCCCCTGGTC	GAATCTGGCG	ATGGCTGTTT
	251	TGTGGGGCGT	GGTTTTGGTG	CTGACTCCGT	ATGTCGGTGG	GGCGTATCAG
	301	ATGCCGTTGG	CNCAATGGC	AAACTACNNN	ATTCTGATCA	ATGCGATTCT
35	351	GTNCGCGCTC	AACATCATCC	CCATCTGCC	TTGGGACGGC	GGCATTTTCA
	401	TCGACACCTT	CCTGTCGGCN	AAATANTCGC	AAGCGTTCCG	CAAATCGAA
	451	CCTTATGGGA	CGTGGATTAT	CCNGCTGCTT	ATGCTGACCG	GGTTTTTGGG
	501	TGCGTNTATT	GCACCGATTG	TGCAGCTGGT	GATTGCGTTT	GTGCAGATGT
	551	TCGTCTGA				

This encodes a protein having amino acid sequence <SEQ ID 50>:

40 1 ..RGYTARYWGD NTAEQYGRLT LNPLPHIDLV GTIIVPLLT L MFTPF LFGWA
 51 RPIPIDSRNF RNPRLAWRCV AASGPLSNLA MAVLGWVVLV LTPYVG GAYQ
 101 MPLAQMANYX ILINAILXAL NIIPILPWDG GIFIDTFLSA KXSQA FRKIE
 151 PYGTWIIXLL MLTGVLGAXI APIVQLVIAF VQMFV*

Based on this analysis, it is predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 12

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 51>

50
55

1	ATGAACCTGA	TTTCACGTTA	CATCATCCGT	CAATGGCGG	TTATGGCGGT
51	TTACGCGCTC	CTTGCCCTTC	TCGCTTTGTA	CAGCTTTTTT	GAAATCCTGT
101	ACGAAACCGG	CAACCTCGGC	AAAGGCAGTT	ACGGCATATG	GGAAATGCTG
151	GGCTACACCG	CCCTCAAAT	GCCGCGCCGC	GCCTACGAAC	TGATTCCCCT
201	CGCCGTCTTT	ATCGGCGGAC	TGGTCTCCCT	CAGCCAGCTT	GCCGCGGGCA
251	CGGAACTGAC	CGTCATCAA	GCCAGCGGCA	TGAGACCAA	AAAGCTGCTG
301	TTGATTCTGT	CGCAGTTCGG	TTTTATTTTT	GCTATTGCCA	CCGTCGCGCT
351	CGGCGAATGG	GTTGCGCCCA	CACTGAGCCA	AAAAGCCGAA	AACATCAAAG

401 CCGCCGCCAT CAACGGCAAA ATCAGCACCG GCAATACCGG CCTTTGGCTG
 451 AAAGAAAAAA ACAGCGTGAT CAATGTGCGC GAAATGTTGC CCGACCAT..

This corresponds to the amino acid sequence <SEQ ID 52; ORF112>:

5 1 MNLISRYIIR QMAVMVYAL LAFLALYSFF EILYETGNLG KGSYGIWEML
 51 GYTALKMPAR AYELIPLAVL IGGLVLSLSQL AAGSELTVIK ASGMSTKKLL
 101 LILSQFGFIF AIATVALGEW VAPTLSQKAE NIKAAAINGK ISTGNTGLWL
 151 KEKNSVINVR EMLPDH...

Further work revealed further partial nucleotide sequence <SEQ ID 53>:

10 1 ATGAACCTGA TTTCACGTTA CATCATCCGT CAAATGGCGG TTATGGCGGT
 51 TTACGCGCTC CTTCGCTTCC TCGCTTTGTA CAGCTTTTTT GAAATCCTGT
 101 ACGAAACCGG CAACCTCGGC AAAGGCAGTT ACGGCATATG GGAAATGCTG
 151 gGCTACACCG CCCTCAAAAT GCCCGCCCGC GCCTACGAAC TGATTCCCCT
 201 CGCCGTCTTT ATCGGCGGAC TGGTCTCCCT CAGCCAGCTT GCCGCCGGCA
 15 251 GCGAACTGAC CGTCATCAAA GCCAGCGGCA TGAGCACCAA AAAGCTGCTG
 301 TTGATTCTGT CGCAGTTCGG TTTTATTTTT GCTATTGCCA CCGTCGCGCT
 351 CGGCGAATGG GTTGCGCCCA CACTGAGCCA AAAAGCCGAA AACATCAAAG
 401 CCGCCGCCAT CAACGGCAAA ATCAGCACCG GCAATACCGG CCTTTGGCTG
 451 AAAGAAAAAA ACAGCTkAT CAATGTGCGC GAAATGTTGC CCGACCATAC
 501 GCTTTTGGGC ATCAAAATTT GGGCGCGCAA CGATAAAAAC GAATTGGCAG
 20 551 AGGCAGTGGA AGCCGATTCC GCCGTTTGA ACAGCGACGG CAGTTGGCAG
 601 TTGAAAAACA TCCGCCGAG CACGCTTGGC GAAGACAAAG TCGAGGTCTC
 651 TATTGCGGCT GAAGAAAAC GGCCGATTTC CGTCAAACGC AACCTGATGG
 701 ACGTATTGCT CGTCAAACCC GACCAAATGT CCGTCGGCGA ACTGACCACC
 25 751 TACATCCGCC ACCTCCAAAA CAACAGCCAA AACACCCGAA TCTACGCCAT
 801 CGCATGGTGG CGCAAATTGG TTTACCCGCG CGCAGCCTGG GTGATGGCGC
 851 TCGTCGCCTT TGCTTTACC CCGCAAACCA CCCGCCACGG CAATATGGGC
 901 TTAAAACTCT TCGCGGCAT CTGTsTCGGA TTGCTGTTCC ACCTTGCCGG
 951 ACGGCTCTTT GGGTTTACCA GCCAACTCGG...

This corresponds to the amino acid sequence <SEQ ID 54; ORF112-1>:

30 1 MNLISRYIIR QMAVMVYAL LAFLALYSFF EILYETGNLG KGSYGIWEML
 51 GYTALKMPAR AYELIPLAVL IGGLVLSLSQL AAGSELTVIK ASGMSTKKLL
 101 LILSQFGFIF AIATVALGEW VAPTLSQKAE NIKAAAINGK ISTGNTGLWL
 151 KEKNSXINVR EMLPDHTLLG IKIWARNDKN ELAEAVEADS AVLNSDGSWQ
 35 201 LKNIRRTSLG EDKVEVSIAA EENWPISVKR NLMVLLVKP DQMSVGELTT
 251 YIRHLQNSQ NTIRYIAIWW RKLVPAAAW VMALVAFAFT POTTRHGNMG
 301 LKLFGGICXG LLFHLAARLF GFTSQL...

Computer analysis of this amino acid sequence predicts two transmembrane domains.

A corresponding ORF from strain A of *N.meningitidis* was also identified:

Homology with a predicted ORF from *N.meningitidis* (strain A)

40 ORF112 shows 96.4% identity over a 166aa overlap with an ORF (ORF112a) from strain A of *N.meningitidis*:

		10	20	30	40	50	60
	orf112.pep	MNLISRYIIRQMAVMVYALLAFLALYSFFEILYETGNLGKGSYGIWEMLGYTALKMPAR					
45	orf112a	MNLISRYIIRQMAVMVYALLAFLALYSFFEILYETGNLGKGSYGIWEMXGYTALKMXAR					
		10	20	30	40	50	60
		70	80	90	100	110	120
50	orf112.pep	AYELIPLAVLIGGLVLSLSQLAAGSELTVIKASGMSTKKLLLILSQFGFIFAIATVALGEW					
	orf112a	AYELMPLAVLIGGLVXSXSQLAAGSELXVIKASGMSTKKLLLILSQFGFIFAIATVALGEW					
		70	80	90	100	110	120

```

              130      140      150      160
orf112.pep  VAPTLSQKAENIKAAAINGKISTGNTGLWLKEKNSVINVREMLPDH
              |||||:|||||
orf112a     VAPTLSQKAENIKAAAINGKISTGNTGLWLKEKNSIINVREMLPDHTLLGIKIWARNDKN
5           130      140      150      160      170      180

orf112a     ELAEAVEADSAVLNSDGSWQLKNIRRSTLGEDKVEVSIAAEEXWPISVKNRLMDVLLVKP
              190      200      210      220      230      240

```

A partial ORF112a nucleotide sequence <SEQ ID 55> was identified:

```

10      1  ATGAACCTGA  TTTACAGTTA  CATCATCCGT  CAAATGGCGG  TTATGGCGGT
      51  TTACGCGCTC  CTTGCCTTCC  TCGCTTTGTA  CAGCTTTTTT  GAAATCCTGT
     101  ACGAAACCGG  CAACCTCGGC  AAAGGCAGTT  ACGGCATATG  GGAAATGNTG
     151  GGNTACACCG  CCCTCAAAAT  GNCCGCCCGC  GCCTACGAAC  TGATGCCCCCT
     201  CGCCGTCCTT  ATCGGCGGAC  TGGTCTCTNT  CAGCCAGCTT  GCCGCCGGCA
15     251  GCGAACTGAN  CGTCATCAAA  GCCAGCGGCA  TGAGCACCAG  AAAGCTGCTG
     301  TTGATTCTGT  CGCAGTTCGG  TTTTATTTTT  GCTATTGCCA  CCGTCGCGCT
     351  CGGCGAATGG  GTTGCGCCCA  CACTGAGCCA  AAAAGCCGAA  AACATCAAAG
     401  CCGCGGCCAT  CAACGGCAAA  ATCAGTACCG  GCAATACCGG  CCTTTGGCTG
     451  AAAGAAAAAA  ACAGCATTAT  CAATGTGCGC  GAAATGTTGC  CCGACCATAC
20     501  CCTGCTGGGC  ATTAAATCT  GGGCCCGCAA  CGATAAAAC  GAACTGGCAG
     551  AGGCAGTGGA  AGCCGATTCC  GCCGTTTGA  ACAGCGACGG  CAGTTGGCAG
     601  TTGAAAAACA  TCCGCCGCGC  CACGCTTGGC  GAAGACAAAG  TCGAGGTCTC
     651  TATTGCGGCT  GAAGAAAANT  GGCCGATTTC  CGTCAAACGC  AACCTGATGG
     701  ACGTATTGCT  CGTCAAACCC  GACCAAATGT  CCGTCGGCGA  ACTGACCACC
25     751  TACATCCGCC  ACCTCCAAAN  NNACAGCCAA  AACACCCGAA  TCTACGCCAT
     801  CGCATGGTGG  CGCAAATTGG  TTTACCCCGC  CGCAGCCTGG  GTGATGGCGC
     851  TCGTCGCCTT  TGCCTTTACC  CCGCAAACCA  CCCGCCACGG  CAATATGGGC
     901  TTAAAANTCT  TCGGCGGCAT  CTGTCTCGGA  TTGCTGTTCC  ACCTTGCCGG
     951  NCGGCTCTTC  NGGTTTACCA  GCCAACTCTA  CGGCATCCCG  CCCTTCCTCG
30    1001  NCGGCGCACT  ACCTACCATA  GCCTTCGCCT  TGCTCGCCGT  TTGGCTGATA
     1051  CGCAACACAG  AAAAACGCTA  A

```

This encodes a protein having amino acid sequence <SEQ ID 56>:

```

      1  MNLISRYIIR QMAVMAYAL LAFLALYSFF EILYETGNLG KGSYGIWEMX
     51  GYTALKMXAR AYELMPLAVL IGGLVSXSQL AAGSELXVIK ASGMSTKKLL
35    101  LILSQFGFIF AIATVALGEW VAPTLSQKAE NIKAAAINGK ISTGNTGLWL
     151  KEKNSIINVR EMLPDHTLLG IKIWARNDKN ELAEAVEADS AVLNSDGSWQ
     201  LKNIRRSTLG EDKVEVSIAA EEXWPISVKR NLMDVLLVKP DQMSVGELTT
     251  YIRHLQXXSQ NTRIYAIAWW RKLVPAAAW VMALVAFAPT PQTTRHGNMG
     301  LKXFGGICLG LLEHLAAGRLF XFTS QLYGIP PFLXGALPTI AFALLAVWLI
40    351  RKQEK*

```

ORF112a and ORF112-1 show 96.3% identity in 326 aa overlap:

```

orf112a.pep  MNLISRYIIRQMAVMAYALLAFLALYSFFEILYETGNLGKGSYGIWEMXGYTALKMXAR
              |||||:|||||
orf112-1     MNLISRYIIRQMAVMAYALLAFLALYSFFEILYETGNLGKGSYGIWEMLGYTALKMPAR
45
orf112a.pep  AYELMPLAVLIGGLVSXSQLAAGSELXVIKASGMSTKKLLLILSQFGFIFAIATVALGEW
              ||||:|||||
orf112-1     AYELIPLAVLIGGLVLSQLAAGSELTVIKASGMSTKKLLLILSQFGFIFAIATVALGEW
50
orf112a.pep  VAPTLSQKAENIKAAAINGKISTGNTGLWLKEKNSIINVREMLPDHTLLGIKIWARNDKN
              |||||:|||||
orf112-1     VAPTLSQKAENIKAAAINGKISTGNTGLWLKEKNSXINVREMLPDHTLLGIKIWARNDKN
55
orf112a.pep  ELAEAVEADSAVLNSDGSWQLKNIRRSTLGEDKVEVSIAAEEXWPISVKNRLMDVLLVKP
              |||||:|||||
orf112-1     ELAEAVEADSAVLNSDGSWQLKNIRRSTLGEDKVEVSIAAEENWPISVKNRLMDVLLVKP
60
orf112a.pep  DQMSVGELTTYIRHLQXXSQNTRIYAIAWWRKLVYPAAAWVMALVAFAPTPTQTRHGNMG
              |||||:|||||
orf112-1     DQMSVGELTTYIRHLQNNQNTRIYAIAWWRKLVYPAAAWVMALVAFAPTPTQTRHGNMG
orf112a.pep  LKXFGGICLGLLEHLAAGRLFXTS QLYGIP PFLXGALPTIAFALLAVWLIRKQEKRX
              || |||||

```

orf112-1

LKLFGGICXGLLFHLAGRLFGFTSQL

Based on this analysis, it is predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

5 Example 13

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 57>

```

1  ..GCAGTAGCCG AAACCTGCCAA CAGCCAGGGC AAAGGTAAAC AGGCAGGCAG
51  TTCGGTTTCT GTTTCACCTGA AAACCTTCAGG CGACCTTTGC GGCAAACCTCA
101 AAACCACCCCT TAAACCTTTG GTCTGCTCTT TGGTTTCCCT GAGTATGGTA
151 TTGCCTGCCC ATGCCCAAAT TACCACCGAC AAATCAGCAC CTAAAAACCA
201 GCAGGTCGTT ATCCTTAAAA CCAACACTGG TGCCCCCTTG GTGAATATCC
251 AAACCTCCGAA TGGACGCGGA TTGAGCCACA ACCGCTA.TA CGCATTGTGAT
301 GTTGACAACA AAGGGGCGAG GTTAAACAAC GACCGTAACA ATAATCCGTT
351 TGTGGTCAAA GGCAGTGCGC AATTGATTTT GAACGAGGTA CGCGGTACGG
15  401 CTAGCAAACT CAACGGCATC GTTACCGTAG GCGGTCAAAA GGCCGACGTG
451 ATTATTGCCA ACCCCAACGG CATTACCGTT AATGGCGGCG GCTTTAAAAA
501 TGTCGGTTCGG GGCATCTTAA CTACCGGTGC GCCCCAAATC GGCAAAGACG
551 GTGCACTGAC AGGATTTGAT GTGCGTCAAG GCACATTGgA CCGTAGrAGC
601 AGCAGGTTGG AATGATAAAG GCGGAGCmrm yTACACCGGG GTACTTGCTC
20  651 GTGCAGTTGC TTTGCAGGGG AAATTwmnGG GTAAA.AACT GGCGGTTTCT
701 ACCGGTCCTC AGAAAGTAGA TTACGCCAGC GGCGAAATCA GTGCAGGTAC
751 GGCAGCGGGT ACGAAACCGA CTATTGCCCT TGATACTGCC GCACTGGGCG
801 GTATGTACGC CGACAGCATC AACTGATTG CCAATGAAAA AGGCGTAGGC
851 GTCTAA

```

25 This corresponds to the amino acid sequence <SEQ ID 58; ORF114>:

```

1  ..AVAETANSQG KGKQAGSSVS VSLKTSGLDC GKLKTTTLKTL VCSLVSLSMV
51  LPAHAQITTD KSAPKNQVV ILKTNLTGAPL VNIQTPNGRG LSHNRXYAFD
101 VDNKGAVLNN DRNNNPFVVK GSAQLILNEV RGTASKLNGI VTVGGQKADV
151 IIANPNGITV NGGGFKNVGR GILTTGAPQI GKDGALTGFD VVKAHWTVXA
30  201 AGWNDKGGAX YTGVLARAVA LQGKXXGKXL AVSTGPQKVD YASGEISAGT
251 AAGTKPTIAL DTAALGMYA DSITLIANEK GVG*

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Further work revealed the complete nucleotide sequence <SEQ ID 59>:

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1  ATGAATAAAG GTTTACATCG CATTATCTTT AGTAAAAAGC ACAGCACCAT
35  51  GGTTGCAGTA GCCGAAAGGT CCAACAGCCA GGGCAAAGGT AAACAGGCAG
101 GCAGTTCGGT TTCTGTTTCA CTGAAAACCT CAGGCGACCT TTGCGGCAAA
151 CTCAAACCA CCCTTAAAC TTTGGTCTGC TCTTTGGTTT CCCTGAGTAT
201 GGTATTGCCT GCCATGCCC AAATTACCAC CGACAAATCA GCACCTAAAA
251 ACCAGCAGGT CGTTATCCTT AAAACCAACA CTGGTGCCCC CTTGGTGAAT
301 ATCCAAACTC CGAATGGACG CGGATTGAGC CACAACCGCT ATACGCAGTT
40  351 TGATGTTGAC AACAAAGGGG CAGTGTTAAA CAACGACCGT AACAAATAATC
401 CGTTTGTGGT CAAAGGCAGT GCGCAATTGA TTTTGAACGA GGTACGCGGT
451 ACGGCTAGCA AACTCAACGG CATCGTTACC GTAGGCGGTC AAAAGGCCGA
501 CGTGATTATT GCCAACCCCA ACGGCATTAC CGTTAATGGC GGCGGCTTTA
551 AAAATGTCGG TCGGGGCATC TTAACACCG GTGCGCCCCA AATCGGCAAA
45  601 GACGGTGAC TGACAGGATT TGATGTGCGT CAAGGCACAT TGACCGTAGG
651 AGCAGCAGGT TGAATGATA AAGGCGGAGC CGACTACACC GGGGTACTTG
701 CTCGTGCAGT TGCTTTGCAG GGGAAATTAC AGGGTAAAAA CCTGGCGGTT
751 TCTACCGGTC CTCAGAAAGT AGATTACGCC AGCGGCGAAA TCAGTGCAGG
801 TACGGCAGCG GGTACGAAAC CGACTATTGC CCTTGATACT GCCGCACTGG
50  851 GCGGTATGTA CGCCGACAGC ATCACAATGA TTGCCAATGA AAAAGGCGTA
901 GCGGTCAAAA ATGCCGCGAC ACTCGAAGCG GCCAAGCAAT TGATTGTGAC
951 TTCGTGAGGC CGCATTGAAA ACAGCGGCGC CATCGCCACC ACTGCCGACG
1001 GCACCGAAGC TTCACCGACT TATCTCTCCA TCGAAACCAC CGAAAAAGGA
1051 GCGGCAGGCA CATTATCTC CAATGGTGGT CGGATCGAGA GCAAAGGCTT
55  1101 ATTGGTTATT GAGACGGGAG AAGATATCAG CTTGCGTAAC GGAGCCGTGG
1151 TGCAGATAAA CGGCAGTCGC CCAGCTACCA CGGTATTAAA TGCTGGTCAT
1201 AATTTGGTGA TTGAGAGCAA AACTAATGTG AACAAATGCCA AAGGCCCGGC

```

1251 TACTCTGTCTG GCCGACGGCC GTACCGTCAT CAAGGAGGCC AGTATTTCAGA
 1301 CTGGCACTAC CGTATACAGT TCCAGCAAAG GCAACGCCGA ATTAGGCAAT
 1351 AACACACGCA TTACCGGGGC AGATGTTACC GTATTATCCA ACGGCACCAT
 1401 CAGCAGTTCC GCCGTAATAG ATGCCAAAGA CACCGCACAC ATCGAAGCAG
 1451 GCAAACCGCT TTCTTTGGAA GCTTCAACAG TTACCTCCGA TATCCGCTTA
 1501 AACGGAGGCA GTATCAAGGG CGGCAAGCAG CTTGCTTTAC TGGCAGACGA
 1551 TAACATTACT GCCAAAACCTA CCAATCTGAA TACTCCCAGC AATCTGTATG
 1601 TTCATACAGG TAAAGATCTG AATTTGAATG TTGATAAAGA TTTGTCTGCC
 1651 GCCAGCATCC ATTTGAAATC GGATAACGCT GCCCATATTA CCGGCACCAG
 1701 TAAAACCCCTC ACTGCCTCAA AAGACATGGG TGTGGAGGCA GGCTCGCTGA
 1751 ATGTTACCAA TACCAATCTG CGTACCAACT CGGTAATCT GCACATTCAG
 1801 GCAGCCAAAG GCAATATTCA GCTTCGCAAT ACCAAGCTGA ACGCAGCCAA
 1851 GGCTCTCGAA ACCACCGCAT TGCAGGGCAA TATCGTTTCA GACGGCCTTC
 1901 ATGCTGTTTC TGCAGACGGT CATGTATCCT TATTGGCCAA CGGTAATGCC
 1951 GACTTTACCG GTCAACATAC CCTGACAGCC AAGGCCGATG TCAATGCAGG
 2001 ATCGGTTGGT AAAGGCCGTC TGAAAGCAGA CAATACCAAT ATCACTTCAT
 2051 CTTCAGGAGA TATTACGTTG GTTGCCGGA ACGGTATTCA GCTTGGTGAC
 2101 GGAAAACAAC GCAATTCAAT CAACGGAAAA CACATCAGCA TCAAAAACAA
 2151 CGGTGGTAAT GCCGACTTAA AAAACCTTAA CGTCCATGCC AAAAGCGGGG
 2201 CATTGAACAT TCATTCCGAC CGGGCATTGA GCATAGAAAA TACCAAGCTG
 2251 GAGTCTACCC ATAATACGCA TCTTAATGCA CAACACGAGC GGGTAACGCT
 2301 CAACCAAGTA GATGCCTACG CACACCGTCA TCTAAGCATT ACCGGCAGCC
 2351 AGATTTGGCA AAACGACAAA CTGCCTTCTG CCAACAGCT GGTGGCTAAC
 2401 GGTGTATTGG CACTCAATGC GCGTATTCC CAAATTGCCG ACAACACCAC
 2451 GCTGAGAGCG GGTGCAATCA ACCTTACTGC CGGTACCGCC CTAGTCAAGC
 2501 GCGGCAACAT CAATTGGAGT ACCGTTTCGA CCAAACTTTT GGAAGATAAT
 2551 GCCGAATTAA AACCATTGGC CGGACGGCTG AATATTGAAG CAGGTAGCGG
 2601 CACATTAACC ATCGAACCTG CCAACCGCAT CAGTGCAGAT ACCGACCTGA
 2651 GCATCAAAAC AGGCGGAAAA TTGCTGTTGT CTGCAAAAGG AGGAAATGCA
 2701 GGTGCGCCTA GTGCTCAAGT TTCCTCATTG GAAGCAAAAG GCAATATCCG
 2751 TCTGGTTACA GGAGAAACAG ATTTAAGAGG TTCTAAAATT ACAGCCGCTA
 2801 AAAACTTGGT TGTCGCCACC ACCAAAGGCA AGTTGAATAT CGAAGCCGTA
 2851 AACAACCTCAT TCAGCAATTA TTTTCCTACA CAAAAGCGG CTGAACTCAA
 2901 CCAAAAATCC AAAGAAATTGG AACAGCAGAT TGCGCAGTTG AAAAAAGCT
 2951 CGCCTAAAAG CAAGCTGATT CCAACCTGC AAGAAGAAGC CGACCGTCTC
 3001 GCTTTCTATA TTCAAGCCAT CAACAAGGAA GTTAAAGGTA AAAAAACCAA
 3051 AGGCAAGAA TACCTGCAAG CCAAGCTTTC TGACAAAAAT ATTGACTTGA
 3101 TTTCCGCACA AGGCATCGAA ATCAGCGGTT CCGATATTAC CGCTTCCAAA
 3151 AACTGAACC TTCACGCCGC AGGCGTATTG CCAAAGGCAG CAGATTTCAGA
 3201 GGCGGCTGCT ATTCGTATTG ACGGCATAAC CGACCAATAT GAAATTGGCA
 3251 AGCCCACCTA CAAGAGTCAC TACGACAAAG CTGCTCTGAA CAAGCCTTCA
 3301 CGTTTGACCG GACGTACAGG GGTAAGTATT CATGCAGCTG CGGCACTCGA
 3351 TGATGCACGT ATTATTATCG GTGCATCCGA AATCAAAGCT CCCTCAGGCA
 3401 GCATAGACAT CAAAGCCCAT AGTGATATTG TACTGGAGGC TGACAAAAAC
 3451 GATGCTATA CCTTCTTAAA AACCAAAGGT AAAAGCGGCA AAATCATCAG
 3501 AAAAACCAAG TTACCCAGCA CCCGCGACCA CCGTATTATG CCAGCCCCCG
 3551 TCGAGCTGAC CGCCAACGGC ATAACGCTTC AGGCAGGCGG CAACATCGAA
 3601 GCTAATACCA CCCGCTTCAA TGCCCTGCA GGTAAAGTTA CCCTGGTTGC
 3651 GGGTGAAGAG CTGCAACTGC TGGCAGAAGA AGGCATCCAC AAGCAGAGT
 3701 TGGATGTCCA AAAAAGCCGC CGCTTTATCG GCATCAAGGT AGGCAAGAGC
 3751 AATTACGTA AAAACGAACT GAACGAAACC AAATTGCCTG TCCGCGTCTG
 3801 CGCCCAAACT GCAGCCACCC GTTCAGGCTG GGATACCGTG CTGGAAGGTA
 3851 CCGAATTCAA AACCACGCTG GCCGGTGCGG ACATTACGGC AGGTGTAGGC
 3901 GAAAAAGCCC GTGCCGATGC GAAAATTATC CTCAAAGGCA TTGTGAACCG
 3951 TATCCAGTCG GAAGAAAAAT TAGAAACCAA CTCAACCGTA TGGCAGAAAC
 4001 AGGCCGGACG CGGCAGCACT ATCGAAACGC TGAACCTGCC CAGCTTCGAA
 4051 AGCCCTACTC CGCCCAAACT GACCGCCCCC GGTGGCTATA TCGTCGACAT
 4101 TCCGAAAGGC AATTGAAAA CCGAAATCGA AAAGCTGGCC AAACAGCCCG
 4151 AGTATGCCTA TCTGAAACAG CTCCAAGTAG CGAAAAACGT CAACTGGAAC
 4201 CAGGTGCAAC TGGCTTACGA TAAATGGGAC TATAAGCAGG AAGGCTTAAC
 4251 CAGAGCCGGT GCAGCGATTG TTACCATAAT CGTAACCGCA CTGACTTATG
 4301 GATACGGCGC AACCGCAGCG GGCGGTGTAG CCGCTTCAGG AAGTAGTACA
 4351 GCCGAGCTG CCGGAACAGC CGCCACAACG ACAGCAGCAG CTACTACCGT
 4401 TTCTACAGCG ACTGCCATGC AAACCGCTGC TTTAGCCTCC TTGTATAGCC
 4451 AAGCAGCTGT ATCCATCATC AATAATAAAG GTGATGTCGG CAAAGCGTTG
 4501 AAAGATCTCG GCACCACTGA TACGGTCAAG CAGATTGTCA CTTCTGCCCT
 4551 GACGGCGGGT GCATTAAATC AGATGGGCGC AGATATTGCC CAATTGAACA
 4601 GCAAGGTAAG AACCGAACTG TTCAGCAGTA CGGGCAATCA AACTATTGCC
 4651 AACCTTGGAG GCAGACTGGC TACCAATCTC AGTAATGCAG GTATCTCAGC
 4701 TGGTATCAAT ACCGCCGTCA ACGGCGGCAG CCTGAAAGAC AACTTAGGCA
 4751 ATGCCGATT AGGAGCATTG GTTAATAGCT TCCAAGGAGA AGCCGCCAGC
 4801 AAAATCAAAA CAACCTTCAG CGACGATTAT GTTGCCAAAC AGTTCGCCCA

5 4851 CGCTTTGGCT GGGTGTGTTA GCGGATTGGT ACAAGGAAAA TGTAAAGACG
 4901 GGGCAATTGG CGCAGCAGTT GGGGAAATCG TAGCCGACTC CATGCTTGGC
 4951 GGCAGAAACC CTGCTACACT CAGCGATGCG GAAAAGCATA AGGTTATCAG
 10 5001 TTACTCGAAG ATTATTGCCG GCAGCGTGGC GGCACCTAAC GCGCGCGATG
 5051 TGAATACTGC GGCGAATGCG GCTGAGGTGG CGGTAGTGAA TAATGCTTTG
 5101 AATTTTGACA GTACCCCTAC CAATGCGAAA AAGCATCAAC CGCAGAAGCC
 5151 CGACAAAACC GCACTGGAAA AAATTATCCA AGGTATTATG CCTGCACATG
 5201 CAGCAGGTGC GATGACTAAT CCGCAGGATA AGGATGCTGC CATTTGGATA
 10 5251 AGCAATATCC GTAATGGCAT CACAGGCCCG ATTGTGATTA CCAGCTATGG
 5301 GGGTTATGCT GCAGGTTGGA CAGCTCCGCT GATCGGTACA GCGGGTAAAT
 5351 TAGCTATCAG CACCTGCATG GCTAATCCTT CTGGTTGTAC TGTCTATGGT
 5401 ACTCAGGCTG CCGAAGCGGG CGCGGGAATC GCCACGGGTG CGGTAACGGT
 5451 AGGCAACGCT TGGGAAGCGC CTGTGGGGGC GTTGTGCGAA GCGAAGGCGG
 15 5501 CCAAGCAGGC TATACCAACC CAGACAGTTA AAGAACTTGA TGGCTTACTA
 5551 CAAGAATCAA AAAATATAGG TGCTGTAAAT ACACGAATTA ATATAGCGAA
 5601 TAGTACTACT CGATATACAC CAATGAGACA AACGGGACAA CCGGTATCTG
 5651 CTGGCTTTGA GCATGTTCTT GAGGGGCACT TCCATAGGCC TATTGCGAAT
 20 5701 AACCGTTCAG TTTTACCAT CTCCCCAAT GAATTGAAGG TTATACTTCA
 5751 AAGTAATAAA GTAGTTTCTT CTCCCGTATC GATGACTCCT GATGGCCAAT
 5801 ATATGCGGAC TGTCGATGTA GGAAAAGTTA TTGGTACTAC TTCTATTAAA
 5851 GAAGGTGGAC AACCACAAAC TACAATTAAA GTATTTACAG ATAAGTCAGG
 5901 AAATTTGATT ACTACATACC CAGTAAAGG AAATAA

This corresponds to the amino acid sequence <SEQ ID 60; ORF114-1>:

25 1 MNKGLHRIIF SKKHSTMVAV AETANSQKG KQAGSSVSVS LKTSGLDCGK
 51 LKTTLLKTLVC SLVLSLMVLP AHAQITTDKS APKNQQVIL KTNTGAPLVN
 101 IQTPNGRGLS HNRYTQFDVD NKGAVLNNDR NNNPFVVKGS AQLILNEVRG
 151 TASKLNGIVT VGGQKADVII ANPNGITVNG GGFKNVGRGI LTTGAPQIGK
 201 DGALTGFVDV QGTLTVGAAG WNDKGGADYT GVLAARVALQ GKLGKNLAV
 251 STGPQKVDYA SGEISAGTAA GTKPTIALDT AALGGMYSADS ITLIANEKGV
 30 301 GVKNAGTLEA AKQLIVTSSG RIENSGRIAT TADGTEASPT YLSIETTEKG
 351 AAGTFISNGG RIESKGLLVI ETGEDISLRN GAVVQNNNGSR PATTVLNLNAGH
 401 NLVIESKTNV NNAKGPAATLS ADGRTVIKEA SIQTGTTVYS SSKGNAELGN
 451 NTRITGADV T VLSNGTISSS AVIDAKDTAH IEAGKPLSLE ASTVTSDIRL
 501 NGGSIKGGKQ LALLADDNIT AKTTNLNTPG NLYVHTGKDL NLNVDKDLSA
 35 551 ASIHLSKSDNA AHITGTSKTL TASKDMGVEA GSLNVTNTNL RTNSGNLHIQ
 601 AAKGNIQLRN TKLNAAKALE TTALQGNIVS DGLHAVSADG HVSLLANGNA
 651 DFTGHNTLTA KADVNAAGSVG KGRKADNTN ITSSSGDITL VAGNGIQLGD
 701 GKQRNSINGK HISIKNNGGN ADLKNLNVHA KSGALNIHSD RALSIENTKL
 751 ESTHNTLNA QHERVTNLQV DAYAHRHLSI TGSQIWQNDK LPSANKLVAN
 40 801 GVLALNARYS QIADNTTLRA GAINLTAGTA LVKRGNNINWS TVSTKTLEDN
 851 AELKPLAGRL NIEAGSGTLT IEPANRISAH TDLSIKTGGK LLLSAKGGNA
 901 GAPSAQVSSL EAKGNIRLVT GETDLRGSKI TAGKNLVVAT TKGKLNIEAV
 951 NNSFSNYFPT QKAAELNQKS KELEQQIAQL KKSSPKSKLI PTLQEERDL
 1001 AFYIQAINKE VKGKKPKGKE YLQAKLSAQN IDLISAQGIE ISGSDITASK
 45 1051 KLNLAAGVL PKAADSEAAA ILIDGITDQY EIGKPTYKSH YDKAALNKPS
 1101 RLTRGTGVSII HAAAALDDAR IIGASEIKA PSGSIDIKAH SDIVLEAGQN
 1151 DAYTFLKTKG KSGKIIRKTK FTSTRDHLIM PAPVELTANG ITLQAGGNIE
 1201 ANTTRFNAPA GKVTLVAGEE LQLLAEEGIH KHELDVQKSR RFIGIKVGKS
 1251 NYSKNELNET KLPVRVVAQT AATRSWDTV LEGTEFKTTL AGADIQAGVG
 50 1301 EKARADAKII LKGIVNRIQS EEKLETNSTV WQKQAGRGST IETLKLPSFE
 1351 SPTPPKLTAP GGYIVDIPKG NLKTEIEKLA KQPEYAYLKQ LQVAKNVNWN
 1401 QVQLAYDKWD YKQEGLTRAG AAIVTIIVTA LTYGYGATAA GGVAASGSST
 1451 AAAAGTAATT TAAATTVSTA TAMQTAALAS LYSQAASVSI NNKGDVGKAL
 1501 KDLGTSDTV K QIVTSALTAG ALNQMGADIA QLNSKVRTEL FSSTGNQTIA
 55 1551 NLGGRLATNL SNAGISAGIN TAVNGGSLKD NLGNAALGAL VNSFQGEAAS
 1601 KIKTTFSDDY VAKQFAHALA GCVSGLVQGK CKDGAIGAAV GEIVADSMLG
 1651 GRNPATLSDA EKHKVISYSK I IAGSVAALN GGDVNTAANA AEVAVVNNAL
 1701 NFDSTPTNAK KHQPQKPKDKT ALEKIIQGIM PAHAAGAMTN PQDKDAIWI
 1751 SNIRNGITGP IVITSYGVYA AGWTAPLIGT AGKLAISTCM ANPSGCTVMV
 60 1801 TQAAEAGAGI ATGAVTVGNA WEAPVGALSK AKAQKQAIPT QTVKELDGLL
 1851 QESKNIGAVN TRINIANSTT RYTPMRQTGO PVSAGFEHVL EGHFHRPIAN
 1901 NRSVFTISPN ELKVILQSNK VVSSPVSMTD DGQYMRVTDV GKVIGTTSIK
 1951 EGGQPTTTIK VFTDKSGNLI TTPVKGN*

Computer analysis of this amino acid sequence predicts a transmembrane region and also gives the

65 following results:

Homology with a predicted ORF from *N.meningitidis* (strain A)

ORF114 shows 91.9% identity over a 284aa overlap with an ORF (ORF114a) from strain A of *N. meningitidis*:

5	orf114.pep		10	20	30	40
			AVAETANSQKGKQAGSSVSVSLKTS	SGDLCGKLKTTLKT	LVC	
10	orf114a	MNKGLHRIIFS	KKHSTMVAVAETANSQKGKQAGSSVSVSLKTS	SGDLCGKLKTTLKT	LVC	
		10	20	30	40	50
15	orf114.pep	50	60	70	80	90
		SLVSLSMVLP	PAHAQITTDKSAPKNQ	QVVLKTN	TGAPLVNIQT	PNGRGLSHNRXYAFD
20	orf114a	50	60	70	80	90
		SLVSLSMXXXXX	QITTDKSAPKNQ	QVVLKTN	TGAPLVNIQT	PNGRGLSHNRXYQFD
25	orf114.pep	110	120	130	140	150
		NKGAVLNND	RNNNPFVVK	GSAQLILNEVR	GTASKLNGIV	TG
30	orf114a	110	120	130	140	150
		NKGAVLNND	RNNNPFVVK	GSAQLILNEVR	GTASKLNGIV	TG
35	orf114.pep	170	180	190	200	210
		GGFKNVGR	GILTTGAPQIG	KDGALTGF	DVVKAHWT	VXAAGW
40	orf114a	170	180	190	200	210
		GGFKNVGR	GILTTGAPQIG	KDGALTGF	DVVKAHWT	VXAAGW
45	orf114.pep	230	240	250	260	270
		GKXXGKX	LAVSTGPQ	KVDYASGE	ISAGTAAG	TKPTIALD
50	orf114a	230	240	250	260	270
		GKXXGKX	LAVSTGPQ	KVDYASGE	ISAGTAAG	TKPTIALD
55	orf114.pep	290	300	310	320	330
		GVX				
60	orf114a	290	300	310	320	330
		GVX				

The complete length ORF114a nucleotide sequence <SEQ ID 61> is:

40	1	ATGAATAAAG	GTTTACATCG	CATTATCTTT	AGTAAAAAGC	ACAGCACCAT
	51	GGTTGCAGTA	GCCGAAACTG	CCAACAGCCA	GGGCAAAGGT	AAACAGGCAG
45	101	GCAGTTCGGT	TTCTGTTTCA	CTGAAACTT	CAGGCGACCT	TTGCGGCAAA
	151	CTCAAAACCA	CCCTTAAAC	CTTGGTCTGC	TCTTTGGTTT	CCCTGAGTAT
50	201	GGNATTNCNN	NNCNTNCCC	AAATTACCAC	CGACAAATCA	GCACCTAAAA
	251	ACCANCAGGT	CGTTATCCTT	AAAACCAACA	CTGGTGCCCC	CTTGGTGAAT
55	301	ATCCAAACTC	CGAATGGACG	CGGATTGAGC	CACAACCGCT	ATACGCAGTT
	351	TGATGTTGAC	AACAAAGGGG	CAGTGTTAAA	CAACGACCGT	AACAATAATC
60	401	CGTTTCTGGT	CAAAGGCAGT	GCGCAATTGA	TTTTGAACGA	GGTACGCGGT
	451	ACGGCTAGCA	AACTCAACGG	CATCGTTACC	GTAGGCGGTC	AAAAGGCCGA
65	501	CGTGATTATT	GCCAACCCCA	ACGGCATTAC	CGTTAATGGC	GGCGGCTTTA
	551	AAAATGTCCG	TCGGGGCATC	TTAACTATCG	GTGCGCCCCA	AATCGGCAAA
70	601	GACGGTGAC	TGACAGGATT	TGATGTGCGT	CAAGGCACAT	TGACCGTAGG
	651	AGCAGCAGGT	TGGAATGATA	AAGGCGGAGC	CGACTACACC	GGGGTACTTG
75	701	CTCGTGCACT	TGCTTTGCAG	GGGAAATTAC	AGGGTAAAAA	CCTGGCGGTT
	751	TCTACCGGTC	CTCAGAAAGT	AGATTACGCC	AGCGGCGAAA	TCAGTGCAGG
80	801	TACGGCAGCG	GGTACGAAAC	CGACTATTGC	CCTTGATACT	GCCGCACTGG
	851	GCGGTATGTA	CGCCGACAGC	ATCACACTGA	TGCCCANTGA	AAAAGGCGTA
85	901	GGCGTCAAAA	ATGCCGGCAC	ACTCGAAGCG	GCCAAGCAAT	TGATTGTGAC
	951	TTCGTCAGGC	CGCATTGAAA	ACAGCGGCCG	CATCGCCACC	ACTGCCGACG
90	1001	GCACCGAAGC	TTACCGGACT	TATCTNNCNA	TCGAAACCAC	CGAAAAAGGA
	1051	GCNNCAGGCA	CATTTATCTC	CAATGGTGGT	CGGATCGAGA	GCAAAGGCTT
95	1101	ATTGGTTATT	GAGACGGGAG	AAGATATCAN	CTTGCGTAAC	GGAGCCGTGG
	1151	TGCAGAATAA	CGGCAGTCGC	CCAGCTACCA	CGGTATTAAA	TGCTGGTCAT
100	1201	AATTTGGTGA	TTGAGAGTAA	AACTAATGTG	AACAATGCCA	AAGGCTCGNC

1251 TAATCTGTCG GCCGGCGGTC GTACTACGAT CAATGATGCT ACTATTCAAG
 1301 CGGGCAGTTC CGTGTACAGC TCCACCAAAG GCGATACTGA NTTGGGTGAA
 1351 AATACCCGTA TTATTGCTGA AAACGTAACC GTATTATCTA ACGGTAGTAT
 1401 TGGCAGTGTG GCTGTAATTG AGGCTAAAGA CACTGCACAC ATTGAAATCGG
 1451 GCAAACCGCT TTCTTTAGAA ACCTCGACCG TTGCCCTCAA CATCCGTTTG
 1501 AACAAACGGTA ACATTAAAGG CGGAAAGCAG CTTGCTTTAC TGGCAGACGA
 1551 TAACATTACT GCCAAACTA CCAATCTGAA TACTCCCGGC AATCTGTATG
 1601 TTCATACAGG TAAAGATCTG AATTTGAATG TTGATAAAGA TTTGTCTGCC
 1651 GCCAGCATCC ATTTGAAATC GGATAACGCT GCCCATATTA CCGGCACCAG
 1701 TAAAACCCCTC ACTGCCTCAA AAGACATGGG TGTGGAGGCA GGCTTGCTGA
 1751 ATGTTACCAA TACCAATCTG CGTACCAACT CGGGTAATCT GCACATTCAG
 1801 GCAGCCAAAG GCAATATTCA GCTTCGCAAT ACCAAGCTGA ACGCAGCCAA
 1851 GGCTCTCGAA ACCACCGCAT TGCAGGGCAA TATCGTTTCA GACGGCCTTC
 1901 ATGCTGTTTC TGCAGACGGT CATGTATCCT TATTGGCCAA CGGTAATGCC
 1951 GACTTTACCG GTCACAATAC CCTGACAGCC AAGGCCGATG TCNATGCAGG
 2001 ATCGGTTGGT AAAGGCCGTC TGAAGCAGA CAATACCAAT ATCACTTCAT
 2051 CTTCAGGAGA TATTACGTTG GTTGCCGNNN NCGGTATTCA GCTTGGTGAC
 2101 GGAAACAAAC GCAATTTCAAT CAACGGAAAA CACATCAGCA TCAAAAACAA
 2151 CGGTGGTAAT GCCGACTTAA AAAACCTTAA CGTCCATGCC AAAAGCGGGG
 2201 CATTGAACAT TCATTCCGAC CGGGCATTGA GCATAGAAAA TACNAAGCTG
 2251 GAGTCTACCC ATAATACGCA TCTTAATGCA CAACACGAGC GGGTAACGCT
 2301 CAACCAAGTA GATGCCACG CACACCGTCA TCTAAGCATT ANCGGCAGCC
 2351 AGATTTGGCA AAACGACAAA CTGCCTTCTG CCAACAAGCT GGTGGCTAAC
 2401 GGTGTATTGG CANTCAATGC GCGCTATTCC CAAATGCCG ACAACACCAC
 2451 GCTGAGAGCG GGTGCAATCA ACCTTACTGC CGGTACCGCC CTAGTCAAGC
 2501 GCGGCAACAT CAATTGGAGT ACCGTTTCGA CCAAGACTTT GGAAGATAAT
 2551 GCCGAATTAA AACCATTGGC CGGACGGCTG AATATTGAAG CAGGTAGCGG
 2601 CACATTAAAC ATCGAACCTG CCAACCGCAT CAGTGCATCAT ACCGACCTGA
 2651 GCATCAAAAC AGGCGGAAAA TTGCTGTTGT CTGCAAAAGG AGGAAATGCA
 2701 GGTGCGCNTA GTGCTCAAGT TTCCTCATTG GAAGCAAAAG GCAATATCCG
 2751 TCTGGTTACA GGAGNAACAG ATTTAAGAGG TTCTAAAATT ACAGCCGGTA
 2801 AAAACTTGGT TGTCCGCACC ACCAAAGGCA AGTTGAATAT CGAAGCGGTA
 2851 AACAACATCAT TCAGCAATTA TTTTCNTACA CAAAAAGNGN NNGNNCTCAA
 2901 CCAAAAATCC AAAGAATTGG AACAGCAGAT TGCAGAGTGA AAAAAAGCT
 2951 CGCNTAAAAG CAAGCTGATT CCAACCCTGC AAGAAGAACG CGACCGTCTC
 3001 GCTTTCTATA TTCAAGCCAT CAACAAGGAA GTTAAAGGTA AAAAACCCAA
 3051 AGGCAAAAGAA TACCTGCAAG CCAAGCTTTC TGCACAAAAT ATTGACTTGA
 3101 TTTCCGCACA AGGCATCGAA ATCAGCGGTT CCGATATTAC CGCTTCCAAA
 3151 AAAGTGAACC TTCACGCCGC AGGCGTATTG CCAAAGGCAG CAGATTGAGA
 3201 GCGCGCTGCT ATTCTGATTG ACGGCATAAC CGACCAATAT GAAATTGGCA
 3251 AGCCACCTA CAAGAGTCAC TACGACAAAG CTGCTCTGAA CAAGCCTTCA
 3301 CGTTTGACCG GACGTACGGG GGTAAGTATT CATGCAGCTG CGGCACTGCA
 3351 TGATGCACGT ATTATTATCG GTGCATCCGA AATCAAAGCT CCCTCAGGCA
 3401 GCATAGACAT CAAAGCCCAT AGTGATATTG TACTGGAGGC TGGACAAAAC
 3451 GATGCCTATA CCTTCTTANA AACCAAAGGT AAAAGCGGCA NAATNATCAG
 3501 AAAAACNAAG TTTACCAGCA CCNGCGANCA CCTGATTATG CCAGCCCNCG
 3551 TCGAGCTGAC CGCCAACGGT ATCACGCTTC AGGCAGGCGG CAACATCGAA
 3601 GCGAATACCA CCCGCTTCAA TGCCCTGCA GGTAAAGTTA CCCTGGTTGC
 3651 GGGTGAANAG NTGCAACTGC TGGCAGAAGA AGGCATCCAC AAGCACGAGT
 3701 TGGATGTCCA AAAAAGCCGC CGCTTTATCG GCATCAAGGT AGGTNAGAGC
 3751 AATTACAGTA AAAACGAACT GAACGAAACC AAATTGCCGT TCCGCGTCGT
 3801 CGCCCAAANT GCAGCCACCC GTTCAGGCTG GGATACCGTG CTCGAAGGTA
 3851 CCGAATTCAA AACCACGCTG GCCGGTGCCG ACATTACGGC AGGTGTANGC
 3901 GAAAAAGCCC GTGTCGATGC GAAAATTATC CTCAAAGGCA TTGTGAACCG
 3951 TATCCAGTCG GAAGAAAAAT TAGAAACCAA CTCAACCGTA TGGCAGAAAC
 4001 AGGCCGGACG CGGCAGCACT ATCGAAACGC TAAAAC TGCC CAGCTTCGAA
 4051 AGCCCTACTC CGCCCAAATT GTCCGCACCC GCGGNTATA TCGTCGACAT
 4101 TCCGAAAGGC AATCTGAAAA CCGAAATCGA AAAGCTGTCC AAACAGCCCG
 4151 AGTATGCCTA TCTGAAACAG CTCCAAGTAG CGAAAAACAT CAACTGGAAT
 4201 CAGGTGCAGC TTGCTTACGA CAGATGGGAC TACAAACAGG AGGGCTTAAC
 4251 CGAAGCAGGT GCGGCGATTA TCGCACTGGC CGTTACCGTG GTCACCTCAG
 4301 GCGCAGGAAC CGGAGCCGTA TTGGGATTAA ACGGTGCGNC CGCCGCCGCA
 4351 ACCAGTGCAG CATTGCGCTC TTTGGCCAGC CAGGCTTCGG TATCGTTTAT
 4401 CAACAACAAA GCGGATGTCG GCAAAACCTT GAAAGAGCTG GGCAGAGCA
 4451 GCACGGTGAA AAATCTGGTG GTTGCCGCCG CTACCGCAGG CGTAGCCGAC
 4501 AAAATCGGCG CTTCGGCACT GANCAATGTC AGCGATAAGC AGTGGATCAA
 4551 CAACCTGACC GTCAACCTAG CCAATGNCGG GCAGTGCCGC ACTGAttaa

This encodes a protein having amino acid sequence <SEQ ID 62>:

1 MNKGLHRIIF SKKHSTMVAV AETANSQKGK KQAGSSVSVS LKTSGLDCGK

51 LKTTTLKTLVC SLVSLSMXXX XXXQITTDKS APKNXQVVIL KTNTGAPLVN
 101 IQTPNGRGLS HNRYTQFDVD NKGAVLNNDNR NNNPFLVKGS AQLILNEVRG
 151 TASKLNGIVT VGGQKADVII ANPNGITVNG GGFKNVGRGI LTIGAPQIGK
 201 DGALTGFVDVR QGTLTVGAAG WNDKGGADYT GVLARAVALQ GKLGKKNLAV
 5 251 STGPQKVDYA SGEISAGTAA GTKPTIALDT AALGGMYSADS ITLIAXEKGV
 301 GVKNAGTLEA AKQLIVTSSG RIENSGRIAT TADGTEASPT YLXIETTEKG
 351 AXGTFFISNGG RIESKGLLVI ETGEDIXLRN GAVVQNNNGSR PATTVLNAGH
 401 NLVIESKTNV NNAKGSXNLS AGGRTTINDA TIQAGSSVYS STKGDTXLGE
 451 NTRIIAENVV VLSNGSIGSA AVIEAKDTAH IESGKPLSLE TSTVASNIRL
 10 501 NNGNIKGGKQ LALLADDNIT AKTTNLNTPG NLYVHTGKDL NLNVDKDLSA
 551 ASIHLSDNA AHITGTSKTL TASKDMGVEA GLLNVTNTNL RTNSGNLHIQ
 601 AAKGNIQLRN TKLNAKALE TTALQGNIVS DGLHAVSADG HVSLLANGNA
 651 DFTGHNTLTA KADVXAGSVG KGRLKADNTN ITSSSGDITL VAXXGIQLGD
 701 GKQRNSINGK HISIKNNGGN ADLKNLNVHA KSGALNIHSD RALSIENTKL
 15 751 ESTHNTLNA QHERVTNLQV DAYAHRHLSI XGSQIWQNDK LPSANKLVAN
 801 GVLAXNARYS QIADNTTLRA GAINLTAGTA LVKRGNIWS TVSTKTLEDN
 851 AELKPLAGRL NIEAGSGTTL IEPANRISAH TDLSIKTGGK LLSAKGGNA
 901 GAXSAQVSSL EAKGNIRLVT GXTDLRSGKI TAGKNLVVAT TKGKLNIEAV
 951 NNSFSNYFXT QKXXXLNQKS KELEQIAQL KKSSXKSKLI PTLQEERDRL
 20 1001 AFYIQAINKE VKGKKPKGKE YLQAKLSAQN IDLISAQGIE ISGSDITASK
 1051 KNLNHAAGVL PKAADSEAAA ILIDGITDQY EIGKPTYKSH YDKAALNKPS
 1101 RLTGRTGVSI HAAAALDDAR IIIGASEIKA PSGSIDIKAH SDIVLEAGQN
 1151 DAYTFLXTKG KSGXXIRKTK FTSTXXHLIM PAPVELTANG ITLQAGGNIE
 1201 ANTTFENAPA GKVTLVAGEX XQLLAEEGIH KHELDVQKSR RFIGIKVXGS
 25 1251 NYSKNEINET KLPVRVVAQX AATRSGWDTV LEGTEFKTTL AGADIQAGVX
 1301 EKARVDAKII LKGIVNRIQS EEKLETNSTV WQKQAGRGST IETLKLPSFE
 1351 SPTPKLSAP GGYIVDIPKG NLKTEIEKLS KQPEYAYLKQ LQVAKNINWN
 1401 QVQLAYDRWD YKQEGLTEAG AAIIALAVTV VTSGAGTGAV LGLNGAXAAA
 1451 TDAAFASLAS QASVSFINNK GDVGKTLKEL GRSTVKNLV VAAATAGVAD
 30 1501 KIGASALXNV SDKQWINNLT VNLANXGQCR TD*

ORF114-1 and ORF114a show 89.8% identity in 1564 aa overlap

orf114a.pep MNKGLHRIIFS KKHSTMVAVAE TANSQKGKQAGSSVSVSLKTSGLDLCGKLTTLKTLVC
 35 orf114-1 MNKGLHRIIFS KKHSTMVAVAE TANSQKGKQAGSSVSVSLKTSGLDLCGKLTTLKTLVC
 orf114a.pep SLVSLSMXXXXXXQITTDKSAPKNXQVVILKTNTGAPLVNIQTTPNGRGLSHNRYTQFDVD
 orf114-1 SLVSLSMVLPAAHQITTDKSAPKNQOVVILKTNTGAPLVNIQTTPNGRGLSHNRYTQFDVD
 40 orf114a.pep NKGAVLNNDNRNNNPFLVKGSAQLILNEVRGTASKLNGIVTVGGQKADVIIANPNGITVNG
 orf114-1 NKGAVLNNDNRNNNPFLVKGSAQLILNEVRGTASKLNGIVTVGGQKADVIIANPNGITVNG
 45 orf114a.pep GGFKNVGRGILTIGAPQIGKDGALTGFVDVRQGTLTVGAAGWNDKGGADYTGVLARAVALQ
 orf114-1 GGFKNVGRGILTIGAPQIGKDGALTGFVDVRQGTLTVGAAGWNDKGGADYTGVLARAVALQ
 orf114a.pep GKLGKKNLAVSTGPQKVDYASGEISAGTAAGTKPTIALDTAALGGMYSADITLIAXEKGV
 50 orf114-1 GKLGKKNLAVSTGPQKVDYASGEISAGTAAGTKPTIALDTAALGGMYSADITLIAXEKGV
 orf114a.pep GVKNAGTLEAAKQLIVTSSGRIENSGRIATTADGTEASPTYLXIETTEKGAXGTFFISNGG
 55 orf114-1 GVKNAGTLEAAKQLIVTSSGRIENSGRIATTADGTEASPTYLSIETTEKGAGTFFISNGG
 orf114a.pep RIESKGLLVIETGEDIXLRNGAVVQNNNGSRPATTVLNAGHNLVIESKTNVNNAKGSXNLS
 orf114-1 RIESKGLLVIETGEDISLRNGAVVQNNNGSRPATTVLNAGHNLVIESKTNVNNAKGPATLS
 60 orf114a.pep AGGRTTINDATI QAGSSVYSSTKGDTXLGENTRIIAENVTVLSNGSIGSAVIEAKDTAH
 orf114-1 ADGRTVIKEASIQGTTVYSSSKGNAELGNTRITGADVTVLSNGTISSSAVIDAKDTAH
 65 orf114a.pep IESGKPLSLETSTVASNIRLNNNGNIKGGKQLALLADDNITAKTTNLNTPGNLYVHTGKDL
 orf114-1 IEAGKPLSLEASTVTSDIRLNGGSIKGGKQLALLADDNITAKTTNLNTPGNLYVHTGKDL
 orf114a.pep NLNVDKDLSAASIHLSDNAAHITGTSKTLTASKDMGVEAGLLNVTNTNLRTNSGNLHIQ
 orf114-1 NLNVDKDLSAASIHLSDNAAHITGTSKTLTASKDMGVEAGLLNVTNTNLRTNSGNLHIQ

	orf114-1	NLNVDKDLAASIHLKSDNAAHITGTSKTLTASKDMGVEAGSLNVTNTNLRNTNSGNLHIQ	
	orf114a.pep	AAKGNIQLRNTKLNAAKALETTALQGNIVSDGLHAVSADGHVSLLANGNADFTGHNTLTA 	
5	orf114-1	AAKGNIQLRNTKLNAAKALETTALQGNIVSDGLHAVSADGHVSLLANGNADFTGHNTLTA	
	orf114a.pep	KADVXAGSVGKGRLLKADNTNITSSSGDITLVAXXGIQLGDGKQRNSINGKHSIKNNGGN 	
10	orf114-1	KADVNAGSVGKGRLLKADNTNITSSSGDITLVAGNGIQLGDGKQRNSINGKHSIKNNGGN	
	orf114a.pep	ADLKNLNVHAKSGALNIHSDRALSIENTKLESTHNTHLNAQHERVTLNQVDAYAHRHLSI 	
	orf114-1	ADLKNLNVHAKSGALNIHSDRALSIENTKLESTHNTHLNAQHERVTLNQVDAYAHRHLSI	
15	orf114a.pep	XGSQIWQNDKLP SANKLVANGVLAXNARYSQIADNTTLRAGAINLTAGTALVKRGNINWS :	
	orf114-1	TGSQIWQNDKLP SANKLVANGVLALNARYSQIADNTTLRAGAINLTAGTALVKRGNINWS	
20	orf114a.pep	TVSTKTLEDNAELKPLAGRLNIEAGSGTLTIEPANRISAHTDLSIKTGGKLLLSAKGGNA 	
	orf114-1	TVSTKTLEDNAELKPLAGRLNIEAGSGTLTIEPANRISAHTDLSIKTGGKLLLSAKGGNA	
	orf114a.pep	GAXSAQVSSLEAKGNIRLVGTGXTDLRGSKITAGKNLVVATTGKGLNIEAVNNSFSNYFXT 	
25	orf114-1	GAPSAQVSSLEAKGNIRLVGTGETDLRGSKITAGKNLVVATTGKGLNIEAVNNSFSNYFFT	
	orf114a.pep	QKXXXLNQKSKELEQQIAQLKKSSXKSKLIPTLQEERDRLAFYIQAINKEVKGKKPKGKE 	
30	orf114-1	QKAAELNQKSKELEQQIAQLKKSSPKSKLIPTLQEERDRLAFYIQAINKEVKGKKPKGKE	
	orf114a.pep	YLQAKLSAQNIDLISAQGIEISGSDITASKKLNLAAGVLPKAADSEAAAAILIDGITDQY 	
	orf114-1	YLQAKLSAQNIDLISAQGIEISGSDITASKKLNLAAGVLPKAADSEAAAAILIDGITDQY	
35	orf114a.pep	EIGKPTYKSHYDKAALNKPSRLTGRTGVSIHAAAALDDARIIIGASEIKAPSGSIDIKAH 	
	orf114-1	EIGKPTYKSHYDKAALNKPSRLTGRTGVSIHAAAALDDARIIIGASEIKAPSGSIDIKAH	
40	orf114a.pep	SDIVLEAGQNDAYTFLXTKGKSGXXIRKTKFTSTXXHLIMPAPVELTANGITLQAGGNIE 	
	orf114-1	SDIVLEAGQNDAYTFLKTKGKSGKIIRKTKFTSTRDHLIMPAPVELTANGITLQAGGNIE	
	orf114a.pep	ANTTRFNAPAGKVTLVAGEXXQLLAEEGIHKHELDVQKSRRFIGIKVGXSNYSKNELNET 	
45	orf114-1	ANTTRFNAPAGKVTLVAGEELQLLAEEGIHKHELDVQKSRRFIGIKVGXSNYSKNELNET	
	orf114a.pep	KLPVRVVAQXAATRSQWDTVLEGTEFKTTLAGADIQAGVXEKARVDAKIIILKGIVNRIQS 	
50	orf114-1	KLPVRVVAQTAATRSQWDTVLEGTEFKTTLAGADIQAGVGEKARADAKIIILKGIVNRIQS	
	orf114a.pep	EEKLETNSTVWQKQAGRGSTIETLKLPSFESPTPPKLSAPGGYIVDIPKGNLKTEIEKLS 	
	orf114-1	EEKLETNSTVWQKQAGRGSTIETLKLPSFESPTPPKLTAPGGYIVDIPKGNLKTEIEKLA	
55	orf114a.pep	KQPEYAYLKQLQVAKNINWNQVQLAYDRWDYKQEGLTEAGAAIIALAVTVVTSAGTGAV 	
	orf114-1	KQPEYAYLKQLQVAKNVNWNQVQLAYDKWDYKQEGLTRAGAAIVTIIIVTALTYGYGATAA	
60	orf114a.pep	LGLNGA-----XAAATD-----AAFASLASQASVSFINNKGDVGKTL 1477 : :: : : : :	
	orf114-1	GGVAASGSSTAAAAGTAATTTAAATTVSTATAMQTAALASLYSQAAVSIINNKGVDGKAL 1500	
	orf114a.pep	KELGRSSTVKNLVVAAATAGVADKIGA-----SALXNVSDKQWINNL-----TVNL 1523 : ::: : : :: : : : :	
65	orf114-1	KDLGTSDTVQKIVTSALTAGALNQMGADIAQLNSKVRTELFSSSTGNQTIANLGGRLATNL 1560	
	orf114a.pep	ANXGQCRTDX :	
70	orf114-1	SNAGISAGINTAVN...	

Homology with pspA putative secreted protein of *N.meningitidis* (accession number AF030941)

ORF114 and pspA protein show 36% aa identity in 302aa overlap:

```

Orf114: 1  AVAETANSQKGKQAGSSVSLSL-----KTSGDXXXXXXXXXXXXXXXXXXXXXPAHAQ 56
          AVAE  +  GK  Q  +  SV  +      S      PA  A
5  pspA:  19  AVAENVHRD GKSMQDSEASVRVTGAASVSSARA AFGFRMAAFSVMLALGVAAFPAPAS 78

Orf114: 57  -ITTDKSAPKNQQVVILKTNTGAPLVNIQTPNGRGLSHNRXYAFDVDNKGAVLNDRNN- 114
          I  DKSAPKNQQ VIL+T  G P VNIQTP+ +G+S NR  FDVD KG +LNN R+N
10 pspA:  79  GIIADKSAPKNQQAVILQTANGLPQVNIQTPSSQGVSVNRFKQFDVDEKGVILNNSRSNT 138

Orf114: 115  -----NPFVVKGSAQLILNEV-RGTASKLNGIVTVGGQKADVIIANPNGITVNGG 163
          NP  +  +G A++I+N++      S LNG  +  VGG++A+V++ANP+GI VNGG
15 pspA:  139  QTQLGGWIQGNPHLARGEARVIVNQIDSSNPSSLNGYIEVGGKRAEVVANPSGIRVNGG 198

Orf114: 164  GFKNVGRGILTGTGAPQIGKDGALTGFDDVKAHWTVXAAGWNDKGGAXYTGVLARAVALQG 223
          G  N      LT+G P  +  +G LTGFDV      +  G  D  A  YT  +L+RA  +
15 pspA:  199  GLINAASVTLTSGVPVL-NNGNLTGFDVSSGKVIGGKGL-DTSDADYTRILSRAAEINA 256

Orf114: 224  KXXGKXLAVSTGPKVDYASGEISAGTAAGTK----PTIALDTAALGGMYADSITLIANE 279
          GK  +  V  +G  K+D+      +A  +      PT+A+DTA LGGMYAD ITLI+  +
20 pspA:  257  GVWGKDVKVVS GKNKLDGSLAKTASAPSSSDSVTPTVAIDTATLGGMYADKITLISTD 316

Orf114: 280  KG 281
          G
25 pspA:  317  NG 318

```

ORF114a is also homologous to pspA:

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gi|2623258 (AF030941) putative secreted protein [Neisseria meningitidis] Length
= 2273
Score = 261 bits (659), Expect = 3e-68
30 Identities = 203/663 (30%), Positives = 314/663 (46%), Gaps = 76/663 (11%)

Query: 1  MNKGLHRIIFSKKHSTMVAVAETANSQKGKQAGSSVSLSLK-----TSGDXXXXXXXXXX 55
          MNK  +++IF+KK S M+AVAE  +  GK  Q  +  SV  +      +S
35 Sbjct: 1  MNKRCYKVIFNKKRSCMMAVAENVHRD GKSMQDSEASVRVTGAASVSSARA AFGFRMAA 60

Query: 56  XXXXXXXXXXXXXXXXXXXXQITTDKSAPKNXQVVILKTNTGAPLVNIQTPNGRGLSHNRYT 115
          I  DKSAPKN Q VIL+T  G P VNIQTP+ +G+S NR+
40 Sbjct: 61  FSVMLALGVAAFPAPASGIIADKSAPKNQQAVILQTANGLPQVNIQTPSSQGVSVNRFK 120

Query: 116  QFDVDNKGAVLNDRNN-----NPFVVKGSAQLILNEV-RGTASKLNGIVTVGG 163
          QFDVD KG +LNN R+N      NP L +G A++I+N++      S LNG  +  VGG
40 Sbjct: 121  QFDVDEKGVILNNSRSNTQTQLGGWIQGNPHLARGEARVIVNQIDSSNPSSLNGYIEVGG 180

Query: 164  QKADVIIANPNGITVNGGGFKNVGRGILTGTGAPQIGKDGALTGFDDVRQGLTVGAAGWND 223
          ++A+V++ANP+GI VNGGG  N      LT G P  +  +G LTGFDV  G  +  +G  G  D
45 Sbjct: 181  KRAEVVVANPSGIRVNGGGLINAASVTLTSGVPVL-NNGNLTGFDVSSGKVIGGKGL-D 238

Query: 224  KGGADYTGVLARAVALQKLGKLNLA VSTGPKVDYASGEISAGTAAGTK----PTIALD 279
          ADYT +L+RA  +  +  GK++ V  +G  K+D+      +A  +      PT+A+D
50 Sbjct: 239  TSDADYTRILSRAAEINAGVWGKDVKVVS GKNKLDGSLAKTASAPSSSDSVTPTVAID 298

Query: 280  TAALGGMYADSITLIAKEKGVGVKNAGTLEAAK-QLIVTSSGRIENSGRIATTADGTEAS 338
          TA LGGMYAD ITLI+  +  G  ++N G  +  AA  +  +++ G++ +A+
55 Sbjct: 299  TATLGGMYADKITLISTDNGAVIRNKGRIFAATGGVTLSDGKLSNSGSI-----DAA 351

Query: 339  PTYLXIETTEKGAXGTFFISNGGRIESKGLLVIIETGEDIXLRNGAVVQNNGSRPATTVLNA 398
          +  +T  +      +  G  I  S  V++  +  I  +  G  +      GS  +  +
60 Sbjct: 352  EITISAQTVD-----NRQGFIRSGKGSVLKVS DGINNQAGLI----GSAGLLDIRDT 399

Query: 399  GHNLVIESKTNVNNAKGS----XNLSAGGRTTINDATI QAGSSVYSSTKGDTXLGENTRI 454
          G  +S  ++NN  G+      ++S  ++  ND  +  A  V  S  +  D  G+
60 Sbjct: 400  G-----KSSLHINNTDGTIIAGKDVSLQAKSLDNDGILTAARDV-SVSLHDDFAGKRDIE 453

Query: 455  IAENVTVLSNGSIGSAAVIEAKDTAHIESGKPLSLETSTVASNIRLNNGNIKGGKQLALL 514
          +T  +  G  +  +  +I+A DT  +  +  +  +  +  S  R      G      L+
65

```

Sbjct: 454 AGRTLTFSTQGR LKNTRIIQAGDTVSLTAAQIDNTVSGKIQSGNRTGLNGKNGITNRGLI 513
 Query: 515 ADDNIT-----AKTTNLNTPGNLYVHTGKDLNLNVDKDLSAASIHLKSDNAAHITGTSKT 569
 + IT AK+ N T G +Y G + + D L+ AA
 5 Sbjct: 514 NSNGITLLQTEAKSDNAGT-GRIY---GSRVAVEADTLLNREETVNGETKAA-----V 562
 Query: 570 LTASKDMGVEAGXXXXXXXXXXXXSGNLHIQAA---KGNIQLRNTKL-NAAKALET TALQ 625
 + A + + + A SG+LHI +A +Q NT L N + A+E++
 10 Sbjct: 563 IAARERLDIGAREIENREAALLSSSGDLHIGSALNGSRQVQGANTSLHNRSAAI ESS--- 619
 Query: 626 GNI 628
 GNI
 Sbjct: 620 GNI 622
 15
 Score = 37.5 bits (85), Expect = 0.53
 Identities = 87/432 (20%), Positives = 159/432 (36%), Gaps = 62/432 (14%)
 20 Query: 239 LQGLQGKNLAVSTGPQKVDYASGEISAGTAAGTKPTIALDTAALGGM YADSITLIA XEK 298
 LQG LQGN+ + G + +G I A A K A + + S T +
 Sbjct: 1023 LQGD LQGNIFAAAGSDITN--TGSIGAENALLK-----ASN NIESRSETRSNQNE 1072
 Query: 299 GVG VKNAGTLEAAKQLIVTSSGRI--ENSGRIATTADGTEASPTYLXIETTEKGAXG-TF 355
 V+N G + A L +G + + I TA E T + G T
 25 Sbjct: 1073 QGSVRNIGRV-AGIYLTGRQNGSVLLDAGNNIVLTAS-----ELTNQSE DGQTV 1120
 Query: 356 ISNGGRIESKGLLV IETGEDIXLRNGAVVQNNGSRPATTVLNAGHNLVIESK-----T 408
 ++ GG I S + I + V++ + +T+ G NL + +K
 30 Sbjct: 1121 LNAGGDIRSDTTGISRNQNTIFDS DNYVIRKEQNEVGSTIRTRG-NLSLNAGD IRIRAA 1179
 Query: 409 NVNNAKG SXNLSAGGR TTINDATI QAGSS-----VYSSTKGDTXLGENTRIIAENV T 460
 V + +G L+AG D ++AG + Y+ G + TR +
 Sbjct: 1180 EVGSEQGR LKLAAG-----RDIKVEAGKAHTETEDALKYTGRSGGGIKQK MTRHLKNQNG 1234
 35 Query: 461 VLSNGSIGSAAVIEAKDTAHIESGKPLSLETSTVASNIRLNNGNIKGGKQLALLADDNIT 520
 +G++ +I +G + + T+ S NN +K + + A+ N
 Sbjct: 1235 QAVSGTLDGKEIILVSGR DITVTGSNIIADNHTILS--AKNNIVLKAAETR SRSAEMNKK 1292
 Query: 521 AKTTNLNTPG-NLYVHTGKDLNLNVDKDLSAASIHLKSDN-----AAHITGTSKTLTA 572
 K+ + + G + KD N + +S + S N H T T T+++
 40 Sbjct: 1293 EKSGLMGSGGIGFTAGSKKDTQTRNSETVSHTESVVGSLNGNTLISAGKHYTQTGSTISS 1352
 Query: 573 SK-DMGVEAGXXXXXXXXXXXXSGNLHIQAAKG-----NIQLRNTKLNAAKALET TALQG 626
 + D+G+ +G + + KG ++ + NT + A A++ G
 45 Sbjct: 1353 PQGDVGISSGKISIDAAQNRY SQESKQVYEQKGVTV AISVPVNTVMGAVDAVKAVQTVG 1412
 Query: 627 NIVSDGLHAVSA 638
 + ++A++A
 50 Sbjct: 1413 KSKNSRVNMAAA 1424

Amino acids 1-1423 of ORF114-1 were cloned in the pGex vector and expressed in *E.coli*, as described above. GST-fusion expression was visible using SDS-PAGE, and Figure 5 shows plots of hydrophilicity, antigenic index, and AMPHI regions for ORF114-1.

Based on these results, including the homology with the putative secreted protein of *N.meningitidis* and on the presence of a transmembrane domain, it is predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 14

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 63>

```

1  ..CGCTTCATTG ATGATGAAGC AGTCGGCAGC AACATCGGCG GCGGCAAAAT
51 GATTGTTGCA GCCGGGCAGG ATATCAATGT ACGCGGCAnA AGCCTTATTT
101 CTGATAAGGG CATTGTTTTA AAAGCAGGAC ACGACATCGA TATTTCTACT
151 GCCCATAATC GCTATACCGG CAATGAATAC CACGAGAGCA wAAAwTCAGG
5 201 CGTCATGGGT ACTGGCGGAT TGGGCTTTAC TATCGGTAAC CGGAAACTA
251 CCGATGACAC TGATCGTACC AATATTGTsC ATACAGGCAG CATTATAGGC
301 AGCCTGAaTG GAGACACCGT TACAGTTGCA GGAAACCGCT ACCGACAAAC
351 CGGCAGTACC GTCTCCAGCC CCGAGGGGCG CAATACCGTC ACAGCCAAAw
401 GCATAGATGT AGAGTTCGCA AACAACCGGT ATGCCACTGA CTACGcCCAT
10 451 ACCCAgGGAA CAAAAAGGCC TTACCGTCGC CCTCAATGTC CCGGTTGTCC
501 AAGCTGCACA AAACCTTCATA CAAGCAGCCC AAAATGTGGG CAAAAGTAA
551 AATAAACGCG TTAATGCCAT GGCTGCAGCC AATGCTGCAT GGCAGAGTTA
601 TCAAGCAACC CAACAAATGC AACAATTTGC TCCAAGCAGC AGTGCGGGAC
651 AAGGTCAAAA CTACAATCAA AGCCCCAGTA TCAGTGTGTC CATTAC.TAC
15 701 GGCGAACAGA AAAGTCGTAA CGAGCAAAAA AGACATTACA CCGAAgCGGC
751 AgCAAGTCAA ATTATCGGCA AAGGGCAAAC CACACTTGCG GCAACAGGAA
801 GTGGGGAGCA GTCCAATATC AATATTACAG GTTCCGATGT CATCGGCCAT
851 GCAGGTACTC C.CTCATTGC CGACAACCAT ATCAGACTCC AATCTGCCAA
901 ACAGGACGGC AGCGAGCAAA GCAAAAACAA AAGCAGTGGT TGGAATGCAG
20 951 GCGTACGTnn CAAATAGGC AACGGCATCA GGTTTGGAAT TACCGCCGGA
1001 GGAAATATCG GTAAAGGTAA AGAGCAAGGG GGAAGTACTA CCCACCGCCA
1051 CACCCATGTC GGCAGCACA CCGGCAAAAC TACCATCCGA AGCGCGGGG
1101 GATACCACCC TCAAAGGTGT GCAGCTCATC GGCAAAGGCA TACAGGCAGA
1151 TACGCGCAAC CTGCATATAG AAAGTGTTCA AGATACTGAA ACCTATCAGA
25 1201 GCAAACAGCA AAACGGCAAT GTCCAAGTTt ACTGTCGGTT ACGGATTCAG
1251 TGCAAGCGGC AGTTACCGCC AAAGCAAAAGT CAAAGCAGAC CATGCCTCCG
1301 TAACCGGGCA AAgCGGTATT TATGCCGGAG AAGACGGCTA TCAAATyAAA
1351 GTyAGAGACA ACACAGACCT yAAGGGCGGT ATCATCACGT CTAGCCAAAG
1401 CGCAGAAGAT AAGGGCAAAA ACCTTTTTCA GACGGCCACC CTTACTGCCA
30 1451 GCGACATTCA AAACCACAGC CGTACGAAG GCAGAAGCTT CGGCATAGGC
1501 GGCAGTTTCG ACCTGAACGG CGGCTGGGAC GGCACGGTTA CCGACAAACA
1551 AGGCAGGCCT ACCGACAGGA TAAGCCCGGC AGCCGGCTAC GGCAGCGACG
1601 GAGACAGCAA AAACAGCACC ACCCGCAGCG GCGTCAACAC CCACACATA
1651 CACATCACCG ACGAAGCGGG ACAACTTGCC CGAACAGGCA GGA CTGCAAA
35 1701 AGAAACCGAA GCGCGTATCT ACACCGGCAT CGACACCGAA ACTGCGGATC
1751 AACACTCAGG CCATCTGAAA AACAGCTTCG AC...

```

This corresponds to the amino acid sequence <SEQ ID 64; ORF116>:

```

1  ..RFIHDEAVGS NIGGGKMIVA AGQDINVRGX SLISDKGIVL KAGHDIDIST
51 AHNRYTGNEY HESXXSGVMG TGGLGFTIGN RKTDDTDRT NIVHTGSIIG
40 101 SLNGDTVTV GNRyRQTGST VSSPEGRNTV TAKXIDVEFA NNRYATDYAH
151 TQEQKGLTVA LNPVVQAAQ NFIQAQNVG KSKNKRNVAM AAANAAWQSY
201 QATQMQQFA PSSSAGQGQN YNQSPSISVS IXYGEQKSRN EQKRHYTEAA
251 ASQIIGKGQT TLAATGSSEQ SNINITGSDV IGHAGTXLIA DNHIRLSAK
301 QDGSEQSKNK SSGWNAGVRX KIGNGIRFGI TAGGNIGKGK EQGGSTTHRH
45 351 THVGSTTGKT TIRSGDRTL KGVQLIGKI QADTRNLHIE SVQDTEYQS
401 KQQNGNVQVT VGYGFSASGS YRQSKVKADH ASVTGQSGIY AGEDGYQIKV
451 RDNTDLKGGI ITSSQSAEDK GKNLFQTATL TASDIQNHRS YEGRSFGIGG
501 SFDLNGGWDG TVTDKQGRPT DRISPAAGYG SDGDSKNSTT RSGVNTNHIH
551 ITDEAGQLAR TGR TAKETEA RIYTGIDTET ADQHSGLHKN SFD...

```

50 Computer analysis of this amino acid sequence gave the following results:

Homology with pspA putative secreted protein of *N.meningitidis* (accession number AF030941)

ORF116 and pspA protein show 38% aa identity in 502aa overlap:

```

Orf116: 6  EAVGSNIGGGKMIVAAGQDINVRGXSLISDKGIVLKAGHDIDISTAHNRYTGNEYHESXX 65
+AV + G ++I+ +G+DI V G ++I+D +L A ++I + A R E ++
55 PspA: 1 235 QAVSGTLDGKEIILVSGRDITVTGSNIIADNHTILSAKNNIVLKAETR SRSAEMNKKEK 1294

Orf116: 66  XXXXXXXXXXXXXXXNRKXXXXXRTNIVHTGSIIGSLNGDTVTVAGNRyRQTGSTVSSPE 125
++K + HT S++GSLNG+T+ AG Y QTGST+SSP+
PspA: 1295 SGLMGSGGIGFTAGSKKDTQTNRSETVSHTESVVGSLNGNTLISAGKHYTQTGSTISSPQ 1354

```

Orf116: 126 GRNTVTAKXIDVEFANNRYATDYAHTQEQKGLTVALNVPXXXX---XXXXXXXXXXXXGKS 182
 G +++ I ++ A NRY+ + EQKG+TVA++VP GKS
 PspA: 1355 GDVGISSGKISIDAAQNRYSQESKQVYEQKGVTVAISVPVNTVMGAVDAVKAVQTVGKS 1414

5 Orf116: 183 KNKRVTXXXXXXXWQSYQATQMQQFA--PSSSAGQGQNYNQSPSISVSIXYGEQKSRN 240
 KN RV + + + A P +AGQG ISVS+ YGEQK+ +
 PspA: 1415 KNSRVNMAAANALNKGVDSGVALYNAARNPKKAAGQG-----ISVSVTYGEQKNTS 1466

10 Orf116: 241 EQKRHYTEAAASQIIGKGQTLAATGSGEQSNINITGSDVIGHAGTXLIADNHRLQSAK 300
 E + T+ +I G G+ +L A+G+G+ S I ITGSDV G GT L A+N +++++A+
 PspA: 1467 ESRIKGTQVQEGKITGGGKVS LTASGAGKDSRITITGSDVYGGKGT RLKAENAVQIEAAR 1526

15 Orf116: 301 QDGSEQSKNKSSGWNAGVRXKIGNGIRFGITAXXXXXXXXXXXXXSTTHRHTHVGGSTTGKT 360
 Q E+S+NKS+G+NAGV I GI FG TA T +R++H+GS +T
 PspA: 1527 QTHQERSENKSAGFNAGVAIAINKGISFGFTAGANYGKGYGNGDETAYRNSHIGSKDSQT 1586

20 Orf116: 361 TIRSGGDTTLKGVQLIGKGIQADTRNLHIESVQDTETYQSKQQNGNVQVTVGYGFSASGS 420
 I SGGDT +KG QL GK+ +LHIES+QDT ++ KQ+N + QVTVGYGFS GS
 PspA: 1587 AIESGGDTVIKGGQLKGKGVGTAESLHIESLQDTAVFKGQENVSAQVTVGYGFSVGGGS 1646

25 Orf116: 421 YRQSKVKADHASVTGQSGIYAGEDGYQIKVRDNTDLKGGIITSSQSAEDKGNLFQTATL 480
 Y +SK +D+ASV QSGI+AG DGY+I+V T L G + S DK KNL +T+ +
 PspA: 1647 YNRKSSSDYASVNEQSGIFAGGDGYRIRVNGKTGLVGAADVSD---ADKSKNLLKTSEI 1703

Orf116: 481 TASDIQNHSRYEGRSFGIGGSF 502
 DIQNH+ + G+ G F
 PspA: 1704 WHKDIQNHASAAASALGLSGGF 1725

Based on homology with *pspA*, it is predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

30 Example 15

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 65>

35 1 ..ACGACCGGCA GCCTCGGCGG CATACTGGCC GGCGGCGGCA CTTCCCTTGC
 51 CGCACCGTAT TTGGACAAAG CGGCGGAAAA CCTCGGTCCG GCGGGCAAAG
 101 CGGCGGTCAA CGCACTGGGC GGTGCGGCCA TCGGCTATGC AACTGGTGGT
 151 AGTGGTGGTG CTGTGGTGGG TCGGAATGTA GATTGGAACA ATAGGCAGCT
 201 GCATCCGAAA GAAATGGCGT TGGCCGACAA ATATGCCGAA GCCCTCAAGC
 251 GCGAAGTTGA AAAACGCGAA GGCAGAAAAA TCAGCAGCCA AGAAGCGGCA
 301 ATGAGAATCC GCAGGCAGAT ATGCGTTGGG TGGACAAAGG TTCCCAAGAC
 351 GGCTATACCG ACCAAAGCGT CATATCCCTT ATCGGAATGA

40 This corresponds to the amino acid sequence <SEQ ID 66; ORF118>:

1 ..TTGSLGGILA GGGTSLAAPY LDKAAENLGP AGKAAVNALG GAAIGYATGG
 51 SGGAVVGANV DWNRRQLHPK EMALADKYAE ALKREVEKRE GRKISSQEAA
 101 MRIRRQICVG WTKVPKTAIP TKASYPLSE*

Computer analysis of this amino acid sequence reveals two putative transmembrane domains.

45 Based on this analysis, it is predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 16

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 67>

1 ..CAATGCCGTC TGAAAAGCTC ACAATTTTAC AGACGGCATT TGTTATGCAA

51 GTACATATAC AGATTCCCTA TATACTGCCC AGrkGCGTGC GTgGCTGAAG
 101 ACACCCCCTA CGCTTGCTAT TTGrAACAGC TCCAAGTCAC CAAAGACGTC
 151 AACTGGAACC AGGTACwACT GGCGTACGAC AAATGGGACT ATAAACAGGA
 201 AGGCTTAACC GGAGCCGGAG CAGCGATTAT TGCCTGGCT GTTACCGTGG
 5 TACTGCGGG CGCGGGAgCC GGAGCCGCAC TGGGcTAAA CGGCGCGGCc
 301 GCAGCGGCAA CCGATGCCCG ATTCCGCTCG CTGGCCAGCC AGGcTTCCGT
 351 ATCGCTCATC AaCAACAAAG GCAATATCGG TAaCACCTG AAAGAGCTGG
 401 GCAGAAGCAG CACGGTGAAG AATCTGATGG TTGCCGTGc tACCGCAgGC
 10 GTagCcgCA AAATCGGTGC TTCGCGACTG AACAAATGTCA GCGATAAGCA
 501 GTGGATCAAC AACCTGACCG TCAACCTGGC CAATGCGGGC AGTGCCGCAC
 551 TGATTAATAC CGCTGTCAAC GGCGGCAGCc tgAAAGACAA TCTGGAAGCG
 601 AATATCCTTG CGGCTTTGGT GAATACTGCG CATGGAGAAG CAGCCAGTAA
 651 AATCAAACAG TTGGATCAGC ACTACATTAC CCACAAGATT GCCCaTGCCA
 15 TAGCGGCTG TGCGGcTGCG GCGGCGAATA AGGGCAAGTG TCAGGATGGT
 751 GCGATAgGTG CGGCTGTGGG CGAGATAGTC GGGGAgGCTT TGACAAACGG
 801 CAAAAATCCT GACACTTTGA CAGCTAAAgA ACGCGaACAG ATTTTGGCAT
 851 ACAGCAAACT GGTTCGGGT ACGGTAAAGC GTGTGGTCGG CGGCGATGTA
 901 AATGCGGCGG CGAATGCGGC TGAGGTAGCG GTGAAAAATA ATCAGCTTAG
 951 CGACAAAtGA

20 This corresponds to the amino acid sequence <SEQ ID 68; ORF41>:

1 ..QCRLKSSQFY RRHLLCKYIY RFPIYCPXAC VAEDTPYACY LXQLQVTKDV
 51 NWNQVXLAYD KWDYKQEGLT GAGAAIALA VTUVTAGAGA GAALINGLAA
 101 AAATDAAFAS LASQASVSLI NNKGNIGNTL KELGRSSTVK NLMVAVATAG
 151 VADKIGASAL NNVSDKQWIN NLTVNLANAG SAALINTAVN GGS�KDNLEA
 201 NILAALVNTA HGEAASKIKQ LDQHYITHKI AHAIAGCAAA AANKGKCQDG
 251 AIGAAVGEIV GEALTNGKNP DTLTAKEREQ ILAYSKLVAG TVSGVVGGDV
 301 NAAANAEEVA VKNNQLSDK*

Further work revealed the complete nucleotide sequence <SEQ ID 69>:

1 ATGCAAGTAA ATATTCAGAT TCCCTATATA CTGCCAGAT GCGTGCGTGC
 30 51 TGAAGACACC CCCTACGCTT GCTATTTGAA ACAGCTCCAA GTCACCAAAG
 101 ACGTCAACTG GAACCAGGTA CAACTGGCGT ACGACAAATG GGACTATAAA
 151 CAGGAAGGCT TAACCGGAGC CGGAGCAGCG ATTATTGCGC TGGCTGTTAC
 201 CGTGGTTACT GCGGGCGCGG GAGCCGGAGC CGCACTGGGC TTAAACGGCG
 251 CGGCCGCAGC GGCAACCGAT GCCGCATTCC CCTCGCTGGC CAGCCAGGCT
 35 301 TCCGTATCGC TCATCAACAA CAAAGGCAAT ATCGGTAACA CCCTGAAAGA
 351 GCTGGGCAGA AGCAGCACGG TGAAAAATCT GATGGTTGCC GTCGCTACCG
 401 CAGGCGTAGC CGACAAAATC GGTGCTTCGG CACTGAACAA TGTCAGCGAT
 451 AAGCAGTGGT TCAACAACCT GACCGTCAAC CTGGCCAATG CGGGCAGTGC
 501 CGCACTGATT AATACCGCTG TCAACGGCGG CAGCCTGAAA GACAATCTGG
 40 551 AAGCGAATAT CCTTGCAGCT TTGGTGAATA CTGCGCATGG AGAAGCAGCC
 601 AGTAAAATCA AACAGTTGGA TCAGCACTAC ATTACCCACA AGATTGCCCA
 651 TGCCATAGCG GGCTGTGCGG CTGCGGCGGC GAATAAGGGC AAGTGTGAGG
 701 ATGGTGCGAT AGGTGCGGCT GTGGGCGAGA TAGTCGGGGA GGCTTTGACA
 751 AACGGCAAAA ATCCTGACAC TTTGACAGCT AAAGAACGCG AACAGATTTT
 45 801 GGCATACAGC AAATCGGTTG CCGGTACGGT AAGCGGTGTG GTCGGCGGCG
 851 ATGTAATGC GCGGCGAAT GCGGCTGAGG TAGCGGTGAA AAAAATCAG
 901 CTTAGCGACA AAGAGGGTAG AGAATTTGAT AACGAAATGA CTGCATGCGC
 951 CAAACAGAAT AATCCTCAAC TGTGCAGAAA AAATACTGTA AAAAAGTATC
 1001 AAAATGTTGC TGATAAAAGA CTGTCTGCTT CGATTGCAAT ATGTACGGAT
 50 1051 ATATCCCCTA GACTGAATG TAGAACAATC AGAAAACAAC ATTTGATCGA
 1101 TAGTAGAAGC CTTATTTCAT CTGGGAAGC AGGTCTAATT GGTAAAGATG
 1151 ATGAATGGTA TAAATTATTC AGCAAATCTT ACACCAAGC AGATTGCGCT
 1201 TTACAGTCTT ATCATTGAA TACTGCTGCT AAATCTTGGC TTCAATCGGG
 55 1251 CAATACAAAG CCTTTATCCG AATGGATGTC CGACCAAGGT TATACACTTA
 1301 TTTCAGGAGT TAATCCTAGA TTCATTCCAA TACCAAGAGG GTTTGTAAAA
 1351 CAAAATACAC CTATTACTAA TGTCAAATAC CCGGAAGGCA TCAGTTTCGA
 1401 TACAAAACCTA AAAAGACATC TGGCAAATGC TGATGGTTTT AGTCAAAAAC
 1451 AGGGCATTAA AGGAGCCCAT AACCGCACCA ATTTTATGGC AGAACTAAAT
 60 1501 TCACGAGGAG GACGCGTAAA ATCTGAAACC CAACTGATA TTGAAGGCAT
 1551 TACCCGAATT AAATATGAGA TTCCTACACT AGACAGGACA GGTAAACCTG
 1601 ATGGTGGATT TAAGGAAATT TCAAGTATAA AAACGTGTTA TAATCCTAAA
 1651 AAATTTTCTG ATGATAAAAT ACTTCAAATG GCTCAAATG CTGCTTCACA
 1701 AGGATATTCA AAAGCCTCTA AAATTGCTCA AAATGAAAGA ACTAAATCAA
 1751 TATCGGAAAG AAAAAATGTC ATTCAATTCT CAGAAACCTT TGACGGAATC
 65 1801 AAATTTAGAT CATATTTTGA TGTAATACA GGAAGAATTA CAAACATTCA
 1851 CCCAGAATAA

This corresponds to the amino acid sequence <SEQ ID 70; ORF41-1>:

```

      1 MQVNIQIPYI LPRCVRAEDT PYACYLKQLQ VTKDVNWNQV QLAYDKWDYK
    51 QEGLTGAGAA IIALAVTVVT AGAGAGAALG LNGAAAAATD AAFASLASQA
   101 SVSLINNKGK IGNTLKEKLG SSVKKNLMVA VATAGVADKI GASALNNVSD
   151 KQWINNLTVN LANAGSAAI NTAVNGGSLK DNLEANILAA LVNTAHGEAA
   201 SKIKQLDQHY ITHKIAHAIA GCAAAAANKG KCQDGAIGAA VGEIVGEALT
   251 NGKNPDTLTA KEREQILAYS KLVAGTVSGV VGGDVNAAAN AAEEVAVKNNQ
   301 LSDKEGREFD NEMTACAKQN NPQLCRKNTV KKYQNVADKR LAASIAICTD
   351 ISRSTECRTI RKQHLIDSR LSHSWEAGLI GKDDWEYKLF SKSYTQADLA
   401 LQSYHLNTAA KSWLQSGNTK PLSEWMSDQG YTLISGVNPR FIPPIRGFVK
   451 QNTPITNVKY PEGISFDTNL KRHLANADGF SQKQGIKGAH NRTNFMALN
   501 SRGGRVKSET QTDIEGITRI KYEIPTLDRG GKPDDGGFKEI SSIKTVYNPK
   551 KFSDDKILQM AQNAASQGY S KASKIAQNER TKSISERKNV IQFSETFDGI
   601 KFRSYFDVNT GRITNIHPE*

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15 Computer analysis of this amino acid sequence predicts a transmembrane domain, and homology with an ORF from *N.meningitidis* (strain A) was also found.

ORF41 shows 92.8% identity over a 279aa overlap with an ORF (ORF41a) from strain A of *N.meningitidis*:

```

20  orf41.pep    10      20      30      40      50      60      69
    orf41a      YRRHLLCKYIYRFPIYCPXACVAEDTPYACYLKQLQVTKDVNWNQVXLAYDKWDYKQEGL
                                || |||||:|::||| ||||:|||||
    orf41a      YLKQLQVAKNINWNQVQLAYDRWDYKQEGL
                                10      20      30

25  orf41.pep    70      80      90      100     110     120     129
    orf41a      TGAGAAIIALAVTVVTAGAGAGAALGLNGAAAAATDAAFASLASQASVSLINNKGKIGNIT
    orf41a      | |||||:|||||:|||||:||||| |||||:|||||:|||||:|
    orf41a      TEAGAAIIALAVTVVTSAGAGTGAVLGLNGAXAAATDAAFASLASQASVSFINNKGKDVGKT
                                40      50      60      70      80      90

30  orf41.pep    130     140     150     160     170     180     189
    orf41a      LKELGRSSTVKKNLMVAVATAGVADKIGASALNNVSDKQWINNLTVNLANAGSAAINTAV
    orf41a      |||||:|||||:|||||:||||| |||||:|||||:|||||:|
    orf41a      LKELGRSSTVKKNLVAAATAGVADKIGASALXNVSDKQWINNLTVNLANAGSAAINTAV
                                100     110     120     130     140     150

35  orf41.pep    190     200     210     220     230     240     249
    orf41a      NGGSLKDNLEANILAAALVNTAHGEAASKIKQLDQHYITHKIAHAIAAGCAAAAANKGKCQD
    orf41a      |||||:|||||:|||||:|||||:|||||:|||||:|
    orf41a      NGGSLKDXLEANILAAALVNTAHGEAASKIKQLDQHYIVHKIAHAIAAGCAAAAANKGKCQD
                                160     170     180     190     200     210

40  orf41.pep    250     260     270     280     290     300     309
    orf41a      GAIGAAVGEIVGEALTNGKNPDTLTAKEREQILAYSKLVAGTVSGVVGGDVNAAANAAEV
    orf41a      |||||:|||||:|||||:|||||:|||||:|||||:|
    orf41a      GAIGAAVGEIVGEALTNGKNPDTLTAKEREQILAYSKLVAGTVSGVVGGDVNAAANAAEV
                                220     230     240     250     260     270

45  orf41.pep    310     320
    orf41a      AVKNNQLSDKX
    orf41a      |||||
    orf41a      AVKNNQLSDXEGREFDNEMTACAKQNXPLCRKNTVKKYQNVADKRLAASIAICTDISRS
                                280     290     300     310     320     330

50  orf41.pep    310     320
    orf41a      AVKNNQLSDKX
    orf41a      |||||
    orf41a      AVKNNQLSDXEGREFDNEMTACAKQNXPLCRKNTVKKYQNVADKRLAASIAICTDISRS
                                280     290     300     310     320     330

```

A partial ORF41a nucleotide sequence <SEQ ID 71> is:

```

55      1 ..TATCTGAAAC AGCTCCAAGT AGCGAAAAAC ATCAACTGGA ATCAGGTGCA
    51      GCTTGCTTAC GACAGATGGG ACTACAAACA GGAGGGCTTA ACCGAAGCAG
   101      GTGCGGCGAT TATCGCACTG GCCGTTACCG TGGTCACCTC AGGCGCAGGA
   151      ACCGGAGCCG TATTGGGATT AAACGGTGCG NCCGCCGCCG CAACCGATGC

```


201 AGCATTCGCC TCTTTGGCCA GCCAGGCTTC CGTATCGTTC ATCAACAACA
 251 AAGGCGATGT CCGCAAAACC CTGAAAGAGC TGGGCAGAAG CAGCAGGCTG
 301 AAAAACTGG TGGTTGCCGC CGCTACCGCA GGCCTAGCCG ACAAATCGG
 351 CGCTTCGGCA CTGANCAATG TCAGCGATAA GCAGTGGATC AACAACTGA
 401 CCGTCAACCT AGCCAATGCG GGCAGTGCCG CACTGATTAA TACCGCTGTC
 451 AACGCGGCA GCCTGAAAGA CANTCTGGAA GCGAATATCC TTGCGGCTTT
 501 GGTCAATACC GCGCATGGAG AAGCAGCCAG TAAAATCAAA CAGTTGGATC
 551 AGCACTACAT AGTCCACAAG ATTGCCCATG CCATAGCGGG CTGTGCGGCA
 601 GCGCGGCGCA ATAAGGGCAA GTGTCAGGAT GGTGCGATAG GTGCGGCTGT
 651 GGGCGAGATA GTCGGGGAGG CTTTGACAAA CCGCAAAAAT CCTGACACTT
 701 TGACAGCTAA AGAACGCGAA CAGATTTTGG CATAACAGCA ACTGGTTGCC
 751 GGTACGGTAA GCGGTGTGGT CCGCGGCGAT GTAAATGCGG CCGCGAATGC
 801 GGCTGAGGTA GCGGTGAAAA ATAATCAGCT TAGCGACNAA GAGGGTAGAG
 851 AATTTGATAA CGAAATGACT GCATGCGCCA AACAGAATAN TCCTCAACTG
 901 TGCAGAAAAA ATACTGTAAA AAAGTATCAA AATGTTGCTG ATAAAAGACT
 951 TGCTGCTTCG ATTGCAATAT GTACGGATAT ATCCCGTAGT ACTGAATGTA
 1001 GAACAATCAG AAAACAACAT TTGATCGATA GTAGAAGCCT TCATTCTACT
 1051 TGGGAAGCAG GTCTAATTGG TAAAGATGAT GAATGGTATA AATTATTAG
 1101 CAAATCTTAC ACCCAAGCAG ATTTGGCTTT ACAGTCTTAT CATTGAATA
 1151 CTGCTGCTAA ATCTTGGCTT CAATCGGGCA ATACAAAGCC TTTATCCGAA
 1201 TGGATGTCCG ACCAAGGTTA TACACTTATT TCAGGAGTTA ATCCTAGATT
 1251 CATTCCAATA CCAAGAGGGT TTGTAAAACA AAATACACCT ATTACTAATG
 1301 TCAAATACCC GGAAGGCATC AGTTTCGATA CAAACCTANA AAGACATCTG
 1351 GCAAATGCTG ATGGTTTTAG TCAAGAACAG GGCATTAAAG GAGCCATAA
 1401 CCGCACCAAT NTTATGGCAG AACTAAATTC ACGAGGAGGA NGNGTAAAT
 1451 CTGAAACCCA NACTGATATT GAAGGCATTA CCCGAATTAA ATATGAGATT
 1501 CCTACACTAG ACAGGACAGG TAAACCTGAT GGTGGATTTA AGGAAATTC
 1551 AAGTATAAAA ACTGTTTATA ATCCTAAAAA NTTTTNNGAT GATAAATAC
 1601 TTCAAATGGC TCAANATGCT GNTTCACAAG GATATTCAA AGCCTCTAAA
 1651 ATTGCTCAA ATGAAAGAAC TAAATCAATA TCGGAAAGAA AAAATGTCAT
 1701 TCAATTCTCA GAAACCTTG ACGGAATCAA ATTTAGANNN TATNTNGATG
 1751 TAAATACAGG AAGAATTACA AACATTACC CAGAATAA

This encodes a protein having the partial amino acid sequence <SEQ ID 72>:

1 YLKQLQVAKN INWNQVQLAY DRWDYKQEGL TEAGAAIAL AVTVVTSAG
 51 TGAVLGLNGA XAAATDAFA SLASQASVSF INNKGDVGKT LKELGRSSTV
 101 KNLVVAATA GVADKIGASA LXNVSDKQWI NNLTVNLANA GSAALINTAV
 151 NGGSLKDXLE ANILAALVNT AHGEAASKIK QLDQHYIVHK IAHAIAAGCAA
 201 AAANKGKCQD GAIGAAVGEI VGEALTNGKN PDTLTAKERE QILAYSKLVA
 251 GTVSGVVGDD VNAANAEEV AVKNNQLSDX EGREFDNEMT ACAKQNXPL
 301 CRKNTVKKYQ NVADKRLAAS IAICTDISRS TECRTIRKQH LIDSRSLHSS
 351 WEAGLIGKDD EWYKLFSKSY TQADLALQSY HLNTAAKSWL QSGNTKPLSE
 401 WMSDQGYTLI SGVNPRFIPI PRGFVKQNTF ITNVKYPEGI SFDTNLXRHL
 451 ANADGFSQEQ GIKGAHNRTN XMAELNSRGG XVKSETXTDI EGITRIKYEI
 501 PTLDRGTGKPD GGFKEISSIK TVYNPKXFXD DKILQMAQXA XSQGYSKASK
 551 IAQNERTKSI SERKNVIQFS ETFDGIKFRX YXDVNTGRIT NIHPE*

ORF41a and ORF41-1 show 94.8% identity in 595 aa overlap:

		10	20	30
50	orf41a.pep	YLKQLQVAKNINWNQVQLAYDRWDYKQEGLTEAGAA		
	orf41-1	MQVNIQIPYILPRCVRAEDTPYACYLKQLQVTKDVNWNQVQLAYDKWDYKQEGLTGAGAA		
		10	20	30
55	orf41a.pep	IIALAVTVVTSAGTGAVALGLNGAXAAATDAAFASLASQASVSFINNKGDVGKTLKELGR		
	orf41-1	IIALAVTVVTAGAGAGAALGLNGAAAAATDAAFASLASQASVSLINNKNIGNTLTKELGR		
		70	80	90
60	orf41a.pep	SSTVKNLVVAATAGVADKIGASALXNVSDKQWNNLTVNLANAGSAAALINTAVNGGSLK		
	orf41-1	SSTVKNLMVAVATAGVADKIGASALNNVSDKQWNNLTVNLANAGSAAALINTAVNGGSLK		
		130	140	150
65	orf41a.pep	DXLEANILAAALVNTAHGEAASKIKQLDQHYIVHKIAHAIAAGCAAAAANKGKCQDGAIGAA		

	or	f41-1	DNLEANILAAALVNTAHGEAASKIKQLDQHYITHKIAHAIAGCAAAAANKGKCQDGAIGAA
			190 200 210 220 230 240
5		or	f41a.pep
			VGEIVGEALTNGKNPDTLTAKEREQILAYSKLVAGTVSGVVGGDVNAAANAEEVAVKNNQ
		or	f41-1
			VGEIVGEALTNGKNPDTLTAKEREQILAYSKLVAGTVSGVVGGDVNAAANAEEVAVKNNQ
10			250 260 270 280 290 300
		or	f41a.pep
			LSDXEGREFDNEMTACAKQNPQLCRKNTVKKYQNVADKRLAASIAICTDISRSTECRTI
		or	f41-1
			LSDXEGREFDNEMTACAKQNPQLCRKNTVKKYQNVADKRLAASIAICTDISRSTECRTI
15			310 320 330 340 350 360
		or	f41a.pep
			RKQHLIDSRSLHSSWEAGLIGKDDWEYKLFKSKSYTQADLALQSYHLNTAAKSWLQSGNTK
20		or	f41-1
			RKQHLIDSRSLHSSWEAGLIGKDDWEYKLFKSKSYTQADLALQSYHLNTAAKSWLQSGNTK
			370 380 390 400 410 420
		or	f41a.pep
			PLSEWMSDQGYTTLISGVNPRFIPIPRGFVKQNTPTITNVKYPEGISFDTNLXRHLANADGF
25		or	f41-1
			PLSEWMSDQGYTTLISGVNPRFIPIPRGFVKQNTPTITNVKYPEGISFDTNLKRHLANADGF
			430 440 450 460 470 480
		or	f41a.pep
			SQEQGIKGAHNRTNXMAELNSRGGXVKSETXTDIEGITRIKYEIPTLDRTGKPDGGFKEI
30		or	f41-1
			SQKQGIKGAHNRTNFMELNSRGGRVKSETQTDIEGITRIKYEIPTLDRTGKPDGGFKEI
			490 500 510 520 530 540
35		or	f41a.pep
			SSIKTVYNPKXFDDKILQMAQXAXSQGYSKASKIAQNERTKSISERKNVIQFSETFDGI
		or	f41-1
			SSIKTVYNPKKFSDDKILQMAQNAASQGYSKASKIAQNERTKSISERKNVIQFSETFDGI
			550 560 570 580 590 600
40		or	f41a.pep
			KFRXYXDVNTGRITNIHPEX
		or	f41-1
			KFRSYFDVNTGRITNIHPEX
45			610 620

Amino acids 25-619 of ORF41-1 were amplified as described above. Figure 6 shows plots of hydrophilicity, antigenic index, and AMPHI regions for ORF41-1.

Based on this analysis, it is predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

50 Example 17

The following DNA sequence was identified in *N.meningitidis* <SEQ ID 73>

	1	ATGGCAATCA	TTACATTGTA	TTATTCTGTC	AATGGTATTT	TAAATGTATG
	51	TGCAAAAGCA	AAAAATATTC	AAGTAGTTGC	CAATAATAAG	AATATGGTTC
	101	TTTTTGGGTT	TTTGGsmrGC	ATCATCGGCG	GTTCAACCAA	TGCCATGTCT
55	151	CCCATATTGT	TAATATTTT	GCTTAGCGAA	ACAGAAAATA	AAAATcgTAT
	201	CGTAAAAATCA	AGCAATCTAT	GCTATCTTTT	GGCGAAAATT	GTTCAAATAT
	251	ATATGCTAAG	AGACCAGTAT	TGGTTATTAA	ATAAGAGTGA	ATACGdTTTA
	301	ATATTTTTAC	TGTCCGTATT	GTCTGTTATT	GGATTGTATG	TTGGAATTCTG
	351	GTTAAGGACT	AAGATTAGCC	CAaATTTTTT	TAAAATGTTA	ATTTTTATTG

401 tTTTATTGGT ATTGGCtCTG AAAATCGGGC AttCGGGTTT AAtCAAActT
451 TAA

This corresponds to the amino acid sequence <SEQ ID 74; ORF51>:

5 1 MAIITLYYSV NGILNCAKA KNIQVVANNK NMVLFGLXX IIGGSTNAMS
51 PILLIFLLSE TENKNRIVKS SNLCYLLAKI VQIYMLRDQY WLLNKSEYXL
101 IFLLSVLSVI GLYVGIRLRT KISPFFKML IFIVLLVLAL KIGHSGLIK
151 *

Further work revealed the complete nucleotide sequence <SEQ ID 75>:

10	1	ATGCAAGAAA	TAATGCAATC	TATCGTTTTT	GTTGCTGCCG	CAATACTGCA
	51	CGGAATTACA	GGCATGGGAT	TTCCGATGCT	CGGTACAACC	GCATTGGCTT
	101	TTATCATGCC	ATTGCTAAG	GTTGTTGCCT	TGGTGGCATT	ACCAAGCCTG
	151	TTAATGAGCT	TGTTGGTCT	ATGCAGCAAT	AACAAAAAGG	GTTTTTGGCA
	201	AGAGATTGTT	TATTATTTAA	AAACCTATAA	ATTGCTTGCT	ATCGGCACGC
15	251	TCGTTGGCAG	CATTTTGGGG	GTGAAGTTGC	TTTTGATACT	TCCAGTGTCT
	301	TGGCTGCTTT	TACTGATGGC	AATCATTACA	TTGTATTATT	CTGTCAATGG
	351	TATTTTAAAT	GTATGTGCAA	AAGCAAAAAA	TATTC AAGTA	GTTGCCAATA
	401	ATAAGAATAT	GGTCTCTTTT	GGGTTTTTGG	CAGGCATCAT	CGGCGGTTCA
	451	ACCAATGCCA	TGTCTCCCAT	ATTGTTAATA	TTTTTGCTTA	CGGAACACAGA
20	501	AAATAAAAAAT	CGTATCGTAA	AATCAAGCAA	TCTATGCTAT	CTTTTGGCGA
	551	AAATTGTTCA	AATATATATG	CTAAGAGACC	AGTATTGGTT	ATTAAATAAG
	601	AGTGAATACG	GTTTAAATAT	TTTACTGTCC	GTATTGTCTG	TTATTGGATT
	651	GTATGTTGGA	ATTCGGTTAA	GGACTAAGAT	TAGCCCAAAT	TTTTTTAAAA
	701	TGTTAAATTTT	TATTGTTTAA	TTGGTATTGG	CTCTGAAAAT	CGGGCATTCTG
	751	GGTTTAAATCA	AACTTTTAA			

25 This corresponds to the amino acid sequence <SEQ ID 76; ORF51-1>:

30

1	<u>MQEIMQSI</u>	<u>VFVAAAILHG</u>	<u>ITGMGF</u>	<u>PMPLGTT</u>	<u>ALAFIMPLSK</u>	<u>VVALVALPSL</u>
51	<u>LMSLLVL</u>	<u>CSNKKGF</u>	<u>WQEI</u>	<u>VYYLKTYKLLA</u>	<u>IGSVVGSILG</u>	<u>VKLLLLILPVS</u>
101	<u>WLLLLMA</u>	<u>ITLYYSV</u>	<u>NGIILN</u>	<u>VCAKAKNIQV</u>	<u>VANNKNMVL</u>	<u>GF</u>
151	<u>TNAMSPILLI</u>	<u>FLLSETENKN</u>	<u>RIVKSSNL</u>	<u>LCYLLAKIVQIYM</u>	<u>LRDQYWLLNK</u>	
201	<u>SEYGLIFLLS</u>	<u>VLSVIGLYVG</u>	<u>IRLRTKISPN</u>	<u>FFKMLIFIVL</u>	<u>LVLALKIGHS</u>	
251	<u>GLIKL</u>	<u>*</u>				

Computer analysis of this amino acid sequence reveals three putative transmembrane domains. A corresponding ORF from strain A of *N.meningitidis* was also identified:

Homology with a predicted ORF from *N.meningitidis* (strain A)

35 ORF51 shows 96.7% identity over a 150aa overlap with an ORF (ORF51a) from strain A of *N.*
meningitidis:

```

10      20      30
orf51.pep      MAITLYYSVNGIILNVCAKAKNIQVVANNK
                ||||||||||||||||||||||||||||
40      orf51a      YKLLAIGSVVGSILGVKLLLLILPVSLLLLMAITLYYSVNGIILNVCAKAKNIQVVANNK
                80      90      100      110      120      130

                40      50      60      70      80      90
orf51.pep      NMVLFGLFLXXIIIGGSTNAMSPILLIFLLSETENKNRIVKSSNLCYLLAKIVQIYMLRDQY
                ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
45      orf51a      NMVLFGLFLAGIIGGSTNAMSPILLIFLLSETENKNRIAKSSNLCYLLAKIVQIYMLRDQY
                140      150      160      170      180      190

                100      110      120      130      140      150
50      orf51.pep      WLLNKSEYXLIFFLLSVLSVIGLYVGIRLRTKISPNNFFKMLIFIVLLVLALKIGHSGLIKL
                ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
orf51a      WLLNKSEYGLIFFLLSVLSVIGLYVGIRLRTKISPNNFFKMLIFIVLLVLALKIGYSGLIKL
                200      210      220      230      240      250

```

ORF51-1 and ORF51a show 99.2% identity in 255 aa overlap:

```

5      orf51a.pep  MQEIMQSIVFVAAAAILHGITGMGFPM LGTTALAFIMPLSKVVALVALPSLLMSLLVLCSN
      orf51-1      MQEIMQSIVFVAAAAILHGITGMGFPM LGTTALAFIMPLSKVVALVALPSLLMSLLVLCSN

      orf51a.pep  NKKGFWEIVYYLKYKLLAIGSVVGSILGVKLLLLILPVSLLLLLMAIITLYYSVNGILN
      orf51-1      NKKGFWEIVYYLKYKLLAIGSVVGSILGVKLLLLILPVSLLLLLMAIITLYYSVNGILN

10     orf51a.pep  VCAKAKNIQVVANNKNMVLFGFLAGIIGGSTNAMSPILLIFLLSETENKNRIAKSSNLCY
      orf51-1      VCAKAKNIQVVANNKNMVLFGFLAGIIGGSTNAMSPILLIFLLSETENKNRIVKSSNLCY

15     orf51a.pep  LLAKIVQIYMLRDQYWLLNKSEYGLIFLLSVLSVIGLYVGIRLRTKISPNFFKMLIFIVL
      orf51-1      LLAKIVQIYMLRDQYWLLNKSEYGLIFLLSVLSVIGLYVGIRLRTKISPNFFKMLIFIVL

      orf51a.pep  LVLALKIGYSGLIKLX
20     orf51-1      LVLALKIGHSGLIK LX

```

The complete length ORF51a nucleotide sequence <SEQ ID 77> is:

```

      1  ATGCAAGAAA TAATGCAATC TATCGTTTTT GTTGCTGCCG CAATACTGCA
      51  CGGAATTACA GGCATGGGAT TTCCGATGCT CGGTACAACC GCATTGGCTT
25     101  TTATCATGCC ATTGTCTAAG GTTGTGCGCT TGGTGGCATT ACCAAGCCTG
      151  TTAATGAGCT TGTGGTCTCT ATGCAGCAAT AACAAAAAGG GTTTTTGGCA
      201  AGAGATTGTT TATTATTTAA AAACCTATAA ATTGCTTGCT ATCGGCAGCG
      251  TCGTTGGCAG CATTTTGGGG GTGAAGTTGC TTTTGATACT TCCAGTGTCT
      301  TGGCTGCTTT TACTGATGGC AATCATTACA TTGTATTATT CTGTCAATGG
30     351  TATTTTAAAT GTATGTGCAA AAGCAAAAAA TATCAAGTA GTTGCCAATA
      401  ATAAGAATAT GGTTCCTTTT GGGTTTTTGG CAGGCATCAT CGGCGGTTC
      451  ACCAATGCCA TGTCTCCCAT ATTGTTAATA TTTTGCTTA GCGAAACAGA
      501  GAATAAAAAAT CGTATCGCAA AATCAAGCAA TCTATGCTAT CTTTGGCAA
      551  AAATTGTTCA AATATATATG CTAAGAGACC AGTATTGGTT ATTAAATAAG
35     601  AGTGAATACG GTTTAATATT TTTACTGTCC GTATTGTCTG TTATTGGATT
      651  GTATGTTGGA ATTCGGTTAA GGAATAAGAT TAGCCCAAAT TTTTAAAAA
      701  TGTTAATTTT TATTGTTTAA TTGGTATTGG CTCTGAAAAT CGGGTATTCA
      751  GGTTAATCA AACTTTAA

```

This encodes a protein having amino acid sequence <SEQ ID 78>:

```

40     1  MQEIMQSIVF VAAAILHGIT GMGFPM LGTT ALAFIMPLSK VVALVALPSL
      51  LMSLLVLCSN NKKGFWEIV YYLKYKLLA IGSVVGSILG VKLLLLILPVS
      101  WLLLLLMAIIT LYYSVNGILN VCAKAKNIQV VANNKNMVLFG FLAGIIGGS
      151  TNAMSPILLI FLLSETENKN RIAKSSNLCY LLAKIVQIYM LRDQYWLLNK
      201  SEYGLIFLLS VLSVIGLYVG IRLRTKISPN FFKMLIFIVL LVLALKIGYS
      251  GLIKL*

```

45 Based on this analysis, it is predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 18

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 79>

```

50     1  ATGAGACATA TGAAAATACA AAATTATTTA CTAGTATTTA TAGTTTTACA
      51  TATAGCCTTG ATAGTAATTA ATATAGTGTT TGGTTATTTT GTTTTCTAT
      101  TTGATTTTTT TGCGTTTTTG TTTTGTGCAA ACGTCTTCTG TGCTGTAAT
      151  TTATTATTTT TAGAAAAAAA CATAAAAAAC AAATTATTGT TTTTATTGCC
      201  GATTTCATTT ATTATATGGA TGGTAATTCA TATTAGTATG ATAAATATAA
55     251  AATTTTATAA ATTTGAGCAT CAAATAAAGG AACAAAATAT ATCCTCGATT
      301  ACTGGGGTGA TAAACCACA TGATAGTTAT AATTATGTTT ATGACTCAA

```

```

351 TGGATATGCT AAATTAAGG ATAATCATAG ATATGGTAGG GTAATTAGAG
401 AAACACCTTA TATTGATGTA GTTGCATCTG ATGTTAAAAA TAAATCCATA
451 AGATTAAAGCT TGGTTTGTGG TATTCATTCA TATGCTCCAT GTGCCAATTT
501 TATAAAATTT GTCAGG..

```

5 This corresponds to the amino acid sequence <SEQ ID 80; ORF82>:

```

1 MRHMKIQNYL LVFIVLHIAL IVINIVFGYF VFLFDFFAFL FFANVFLAVN
51 LLFLEKNIKN KLLFLLPISI IIWMVIHISM INIKFYKFEH QIKEQNISSI
101 TGVIKPHDSY NYVYDSNGYA KLKDNHRYGR VIRETPYIDV VASDVKNKSI
151 RLSLVCGIHS YAPCANFIKF VR..

```

10 Further work revealed the complete nucleotide sequence <SEQ ID 81>:

```

1 ATGAGACATA TGAAAAATAA AAATTATTTA CTAGTATTTA TAGTTTTACA
51 TATAGCCTTG ATAGTAATTA ATATAGTGTG TGGTTATTTT GTTTTTCTAT
101 TTGATTTTTT TCGGTTTTTG TTTTGTCAA ACGTCTTCTT TGCTGTAAAT
151 TTATTATTTT TAGAAAAAAC CATAAAAAAC AAATTATTTG TTTTATTGCC
15 GATTCTATT ATTATATGGA TGGTAATTCA TATTAGTATG ATAAATATAA
251 AATTTTATAA ATTTGAGCAT CAAATAAAGG AACAAAATAT ATCCTCGATT
301 ACTGGGGTGA TAAACCACA TGATAGTTAT AATTATGTTT ATGACTCAAA
351 TGGATATGCT AAATTAAGG ATAATCATAG ATATGGTAGG GTAATTAGAG
401 AAACACCTTA TATTGATGTA GTTGCATCTG ATGTTAAAAA TAAATCCATA
20 AGATTAAAGCT TGGTTTGTGG TATTCATTCA TATGCTCCAT GTGCCAATTT
501 TATAAAATTT GCAAAAAAAC CTGTTAAAT TTATTTTAT AATCAACCTC
551 AAGGAGATTT TATAGATAAT GTAATATTG AAATTAATGA TGGAAACAA
601 AGTTTGTACT TGTTAGATAA GTATAAACA TTTTCTTCTA TTGAAACAG
651 TGTTTGTATC GTATTAAAT TTTTATATT AAAATTTAAT TTGCTTTTAT
25 ATAGGACTTA CTTCAATGAG TTGGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 82; ORF82-1>:

```

1 MRHMKKNKYL LVFIVLHIAL IVINIVFGYF VFLFDFFAFL FFANVFLAVN
51 LLFLEKNIKN KLLFLLPISI IIWMVIHISM INIKFYKFEH QIKEQNISSI
30 TGVIKPHDSY NYVYDSNGYA KLKDNHRYGR VIRETPYIDV VASDVKNKSI
151 RLSLVCGIHS YAPCANFIKF AKKPVKIYFY NQPQGFIDN VIFEINDGNK
201 SLYLLDKYKT FFLIENSVC I VLIILYLKFN LLLYRTYFNE LE*

```

Computer analysis of this amino acid sequence reveals a predicted leader peptide.

A corresponding ORF from strain A of *N.meningitidis* was also identified:

Homology with a predicted ORF from *N.meningitidis* (strain A)

35 ORF82 shows 97.1% identity over a 172aa overlap with an ORF (ORF82a) from strain A of *N.meningitidis*:

```

              10      20      30      40      50      60
orf82.pep    MRHMKIQNYLLVFIVLHIALIVINIVFGYFVFLFDFFAFLFFANVFLAVNLLFLEKNIKN
40 orf82a     MRHMKKNKYL LVFIVLHITLIVINIVFGYFVFLFDFFAFLFFANVFLAVNLLFLEKNIKN
              10      20      30      40      50      60
              70      80      90     100     110     120
orf82.pep    KLLFLLPISIIWMVIHISMINIKFYKFEHQIKEQNISSITGVIKPHDSYNYVYDSNGYA
45 orf82a     KLLFLLPISIIWMVIHISMINIKFYKFEHQIKEQNISSITGVIKPHDSYNYVYDSNGYA
              70      80      90     100     110     120
              130     140     150     160     170
50 orf82.pep  KLKDNHRYGRVIRETPYIDVVASDVKNKSIRLSLVCGIHSYAPCANFIKIFVR
orf82a       KLKDNHRYGRVIRETPYIDVVASDVKNKSIRLSLVCGIHSYAPCANFIKFAKKPVKIYFY
              130     140     150     160     170     180

```

ORF82a and ORF82-1 show 99.2% identity in 242 aa overlap:

```

5  orf82a.pep  MRHMKNKNYLLVFIVLHITLIVINIVFGYFVFLDFFAFLFFANVFLAVNLLFLEKNIKN
    orf82-1    MRHMKNKNYLLVFIVLHIALIVINIVFGYFVFLDFFAFLFFANVFLAVNLLFLEKNIKN

    orf82a.pep  KLLFLLPISIIWMVIHISMINIKFYKFEHQIKEQNISSITGVIKPHDSYNYVYDSNGYA
    orf82-1    KLLFLLPISIIWMVIHISMINIKFYKFEHQIKEQNISSITGVIKPHDSYNYVYDSNGYA

10  orf82a.pep  KLKDNHRYGRVIRETPYIDVVASDVKNKSIRLSLVCGIHSYAPCANFIKFAKKPVKIYFY
    orf82-1    KLKDNHRYGRVIRETPYIDVVASDVKNKSIRLSLVCGIHSYAPCANFIKFAKKPVKIYFY

15  orf82a.pep  NQPQGD FIDNVIFEINDGKKS LYLDDKYKTFFLIENSV CIVLIILYLKFN LLLYRTYFNE
    orf82-1    NQPQGD FIDNVIFEINDGKKS LYLDDKYKTFFLIENSV CIVLIILYLKFN LLLYRTYFNE

    orf82a.pep  LEX
    orf82-1    LEX
20

```

The complete length ORF82a nucleotide sequence <SEQ ID 83> is:

```

25  1  ATGAGACATA TGAAAAATAA AAATTATTTA CTAGTATTTA TAGTTTACATA
    51  TATAACCTTG ATAGTAATTA ATATAGTGTT TGGTTATTTT GTTTTCTAT
    101  TTGATTTTTT TCGGTTTTTG TTTTGTGCAA ACGTCTTCTT TGCTGTAAAT
    151  TTATTATTTT TAGAAAAAAA CATAAAAAAC AAATTATTGT TTTTATTGCC
    201  GATTTCTATT ATTATATGGA TGGTAATTCA TATTAGTATG ATAAATATAA
    251  AATTTTATAA ATTTGAGCAT CAAATAAAGG AACAAAATAT ATCCTCGATT
    301  ACTGGGGTGA TAAAACCACA TGATAGTTAT AATTATGTTT ATGACTCAAA
30  351  TGGATATGCT AAATTAAGAAG ATAATCATAG ATATGGTAGG GTAATTAGAG
    401  AAACACCTTA TATTGATGTA GTTGCATCTG ATGTTAAAAA TAAATCCATA
    451  AGATTAAGCT TGGTTTGTGG TATTCATTCA TATGCTCCAT GTGCCAATTT
    501  TATAAAATTT GCAAAAAAAC CTGTTAAAAT TTATTTTATAT AATCAACCTC
    551  AAGGAGATTT TATAGATAAT GTAATATTG AAATTAATGA TGGAAAAAAA
35  601  AGTTTGTACT GTTAGATAA GTATAAACA TTTTTCCTTA TTGAAAACAG
    651  TGTGTATC GTATTAATTA TTTTATATT AAAATTTAAT TTGCTTTTAT
    701  ATAGGACTTA CTTCAATGAG TTGAATAG

```

This encodes a protein having amino acid sequence <SEQ ID 84>:

```

40  1  MRHMKNKNYL LVFIVLHITL IVINIVFGYF VFLEDDFAFL FFANVFLAVN
    51  LLFLEKNIKN KLLFLLPISI IWMVIHISM INIKFYKFEH QIKEQNISSI
    101  TGVIKPHDSY NYVYDSNGYA KLKDNHRYGR VIRETPYIDV VASDVKNKSI
    151  RLSLVCGIHS YAPCANFIK AKKPVKIYFY NQPQGD FIDN VIFEINDGK
    201  SLYLLDKYKT FFLIENSVCI VLIILYLKFN LLLYRTYFNE LE*

```

Based on this analysis, it is predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 19

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 85>

```

50  1  . . ACCCCCAACA GCGTGACCGT CTTGCCGTCT TTCGGCGGAT TCGGGCGTAC
    51  CGGCGCGACC ATCAATGCAG CAGGCGGGGT CGGCATGACT GCCTTTTCGA
    101  CAACCTTAAT TTCCGTAGCC GAGGGCGCGG TTGTAGAGCT GCAGGCCGTG
    151  AGAGCCAAAG CCGTCAATGC AACCGCCGCT TGCATTTTTA CCGTCTTGAG
    201  TAAGGACATT TTCGATTTC TTTTATTTT CCGTTTTCAG ACGGCTGACT
    251  TCCGCCTGTA TTTTCGCCAA AGCCATGCCG ACAGCGTGCG CCTTGACTTC
    301  ATATTTAAAA GCTTCCGCGC GTGCCAGTTC CAGTTCGCGC GCATAGTTT
55  351  GAGCCGACAA CAGCAGGGCT TCGCCTTGT CGCGCTCCAT CTTGTCGATG

```

```

401   ACCGCCTGCA GCTTCGCAAA TGCCGACTTG TAGCCTTGAT GGTGCGACAC
451   AGCCAAGCCC GTGCCGACAA GCGCGATAAT GGCAATCGGT TGCCAGTAAT
501   TCGCCAGCAG TTTCACGAGA TTCATTCTCG ACCTCCTGAC GCTTCACGCT
551   GA

```

5 This corresponds to the amino acid sequence <SEQ ID 86; ORF124>:

```

1   ..TPNSVTVLPS FGGFGRTGAT INAAGGVGMT AFSTTLISVA EGAVVELQAV
51  RAKAVNATAA CIFTVLSKDI FDFLFIFRFQ TADFRLYFRQ SHADSVRLDF
101 IFKSFRACQF QFARIVLSRQ QQGLRLVALH LVDDRLLQLRK CRLVALMVRH
151 SQARADKRDN GNRLPVIRQQ FHEIHSRPPD ASR*

```

10 Computer analysis of this amino acid sequence predicts a transmembrane domain.

Further work revealed the complete nucleotide sequence <SEQ ID 87>:

```

1   ATGACTGCCT TTTCGACAAC CTTAATTTCC GTAGCCGAGG GCGCGGTTGT
51  AGAGCTGCAG GCCGTGAGAG CCAAAGCCGT CAATGCAACC GCCGCTTGCA
15  101 TTTTACGGT CTTGAGTAAG GACATTTTCG ATTTCTTTT TATTTTCCGT
151 TTTAGACGG CTGACTTCCG CCTGTTTTTT CGCCAAAGCC ATGCCGACAG
201 CGTGCCTT GACTTCATAT TTTTAGCTT CCGCGCGTGC CAGTTCCAGT
251 TCGCGCGCAT AGTTTGTAGC CGACAACAGC AGGGCTTGCG CTTGTGCGG
301 CTCCATCTTG TCGATGACCG CCTGCTGCTT CGCAAATGCC GACTTGTAGC
20  351 CTTGATGGTG CGACACAGCC AAGCCCGTGC CGACAAGCGC GATAATGGCA
401 ATCGGTTGCC AGTTATTCGC CAGCAGTTTC ACGAGATTCA TTCTCGACCT
451 CCTGACGCTT CACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 88; ORF124-1>:

```

1   MTAFTTLIS VAEGAVVELQ AVRRAKAVNAT AACIFTVLSK DIFDFLFIFR
25  51 FQTADFRLEF RQSHADSVRL DFIFFSFRAC QFQFARIVLS RQQQGLRLVA
101 LHLVDDRLLL RKRLVALMV RHSQARADKR DNGNRLPVIR QQFHEIHSRP
151 PDASR*

```

A corresponding ORF from strain A of *N.meningitidis* was also identified:

Homology with a predicted ORF from *N.meningitidis* (strain A)

ORF124 shows 87.5% identity over a 152aa overlap with an ORF (ORF124a) from strain A of *N.meningitidis*:

```

30  orf124.pep   TPNSVTVLPSFGGFGRTGATINAAGGVGMTAFSTTLISVAEGAVVELQAVRAKAVNATAA
      10      20      30      40      50      60
35  orf124a      MTAFTTLISVAEGALVELQAVMAKAVNTTAA
      10      20      30

      70      80      90      100     110     120
40  orf124.pep   CIFTVLSKDIFDFLFIFRFQTADFRLYFRQSHADSVRLDFIFKSFRACQFQFARIVLSRQ
      40      50      60      70      80      90
40  orf124a      CIFTVLSKDIFDFLFIFRFQTADFRLLFRQSHADGVRLDFIFFSFRTRLRQFAGVLSRQ

      130     140     150     160     170     180
45  orf124.pep   QQGLRLVALHVLDDRLLQLRKRLVALMVRHRSQARADKRDNGNRLPVIRQQFHEIHSRPPD
      100     110     120     130     140     150
45  orf124a      QQGLRLVALHFLNDRLLLRSRLVALMVRHRQTRADKRDDGNRLPVIRQQFHEIHSRPPD

50  orf124.pep   ASRX
      :
50  orf124a      VX

```

ORF124a and ORF124-1 show 89.5% identity in 152 aa overlap:

```

    orf124-1.pep  MTAfstTLISVAEGAVVELQAVRAKAVNATAACIFTVLskDIFdFLFIfrFQTADfRLFF
    orf124a      MTAfstTLISVAEGALVELQAVMAKAVNTTAACIFTVLskDIFdFLFIfrFQTADfRLFF

5   orf124-1.pep  RQSHADSVRLDFIFFSFRACQFQFARIVLSRQQQGLRLVALHLVDDRLLLRKCRlVALMV
    orf124a      RQSHADGVRLDFIFFSFRTRLFQFAGVVLSRQQQGLRLVALHFLNDRLLLRKSRLVALMV

10  orf124-1.pep  RHSQARADKRDNGNRLPVIRQQFHEIHSRPPDASRX
    orf124a      RHRQTRADKRDDGNRLPVIRQQFHEIHSRPPDVX

```

The complete length ORF124a nucleotide sequence <SEQ ID 89> is:

```

1   ATGACCGCCT TTCGACAAC CTTAATTTCC GTAGCCGAGG GCGCGCTTGT
51  AGAGCTGCAA GCCGTGATGG CCAAAGCCGT CAATACAACC GCCGCCTGCA
15  101 TTTTACGGT CTGAGTAAG GACATTTTCG ATTTCTTTT TATTTTCCGT
    151 TTTcAGACGG CTGACTTCCG CCTGTTTTT CGCCAAAGCC ATGCCGACGG
    201 CGTGCGCCTT GACTTCATAT TTTTtagCTT CCGCACGCGC CTGTTCCAGT
    251 TCGCGGGCGT AGTTTtGAGC CGACAACAGC AGGGCTTGCG CCTGTGCGG
    301 CTTCATTTTC TCAATGACCG CCTGCTGCTT CGCAAAAGCC GACTTGTAGC
20  351 CTTGATGGTG CGACACCGCC AAACCCGTGC CGACAAGCGC GATGATGGCA
    401 ATCGGTTGCC AGTTATTtGC CAGCAGTTTC ACGAGATTCA TTCTCGACCT
    451 CcTGACGTTT GA

```

This encodes a protein having amino acid sequence <SEQ ID 90>:

```

25  1   MTAfstTLIS VAEGALVELQ AVMAKAVNTT AACIFTVLsk DIFdFLFIfr
    51  FQTADfRLFF RQSHADGVRL DFIffSFRtr LFQFAGVVLS RQQQGLRLVA
    101 LHFLNDRLLL RKSRLVALMV RHRQTRADKR DDGNRLPVIR QQFHEIHSRP
    151 PDV*

```

ORF124-1 was amplified as described above. Figure 7 shows plots of hydrophilicity, antigenic index, and AMPHI regions for ORF124-1.

Based on this analysis, it is predicted that this protein from *N.meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

It will be appreciated that the invention has been described by means of example only, and that modifications may be made whilst remaining within the spirit and scope of the invention.

TABLE I – PCR primers

ORF	Primer	Sequence	Restriction sites
ORF 38	Forward	CGCGGATCCCATATG-TCGCCGCAAATTCGA	BamHI-NdeI XhoI
	Reverse	CCCGCTCGAG-TTTTGCCGCGTTAAAAGC	
ORF 40	Forward	CGCGGATCCCATATG-ACCGTGAAGACCGCC	BamHI-NdeI XhoI
	Reverse	CCCGCTCGAG-CCACTGATAACCGACAGA	
ORF 41	Forward	CGCGGATCCCATATG-TATTTGAAACAGCTCCAAG	BamHI-NdeI XhoI
	Reverse	CCCGCTCGAG-TTCTGGGTGAATGTTA	
ORF 44	Forward	GCGGATCCCATATG-GGCACGGACAACCCC	BamHI-NdeI XhoI
	Reverse	CCCGCTCGAG-ACGTGGGGAACAGTCT	
ORF 51	Forward	GCGGATCCCATATG-AAAAATATTCAAGTAGTTGC	BamHI-NdeI XhoI
	Reverse	CCCGCTCGAG-AAGTTTGATTAAACCCG	
ORF 52	Forward	CGCGGATCCCATATG-TGCCAACGCAATCCG	BamHI-NdeI XhoI
	Reverse	CCCGCTCGAG-TTTTTCAGCTCCGGCA	
ORF 56	Forward	GCGGATCCCATATG-GTTATCGGAATATTACTCG	BamHI-NdeI XhoI
	Reverse	CCCGCTCGAG-GGCTGCAGAAGCTGG	
ORF 69	Forward	CGCGGATCCCATATG-CGGACGTGGTTGGTTTT	BamHI-NdeI XhoI
	Reverse	CCCGCTCGAG-ATATCTTCGTTTTTTTCAC	
ORF 82	Forward	CGCGGATCCGCTAGC-GTAAATTTATTATTTTAGAA	BamHI-NheI XhoI
	Reverse	CCCGCTCGAG-TTCCAATCATTGAAGTA	
ORF 114	Forward	CGCGGATCCCATATG-AATAAAGGTTTACATCGCAT	BamHI-NheI XhoI
	Reverse	CCCGCTCGAG-AATCGCTGCACCGGCT	
ORF 124	Forward	CGCGGATCCCATATG-ACTGCCTTTTCGACA	BamHI-NheI XhoI
	Reverse	CCCGCTCGAG-GCGTGAAGCGTCAGGA	

TABLE II – Cloning, expression and purification

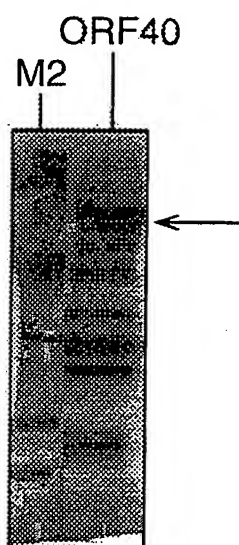
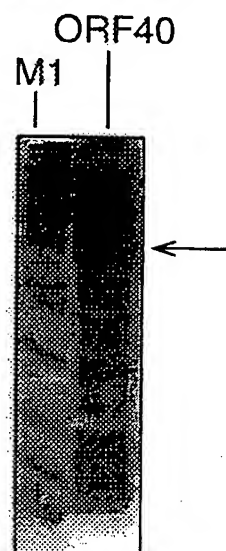
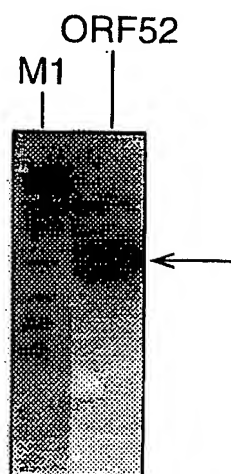
ORF	PCR/cloning	His-fusion expression	GST-fusion expression	Purification
orf 38	+	+	+	His-fusion
orf 40	+	+	+	His-fusion
orf 41	+	n.d.	n.d.	
orf 44	+	+	+	His-fusion
orf 51	+	n.d.	n.d.	
orf 52	+	n.d.	+	GST-fusion
orf 56	+	n.d.	n.d.	
orf 69	+	n.d.	n.d.	
orf 82	+	n.d.	n.d.	
orf 114	+	n.d.	+	GST-fusion
orf 124	+	n.d.	n.d.	

CLAIMS

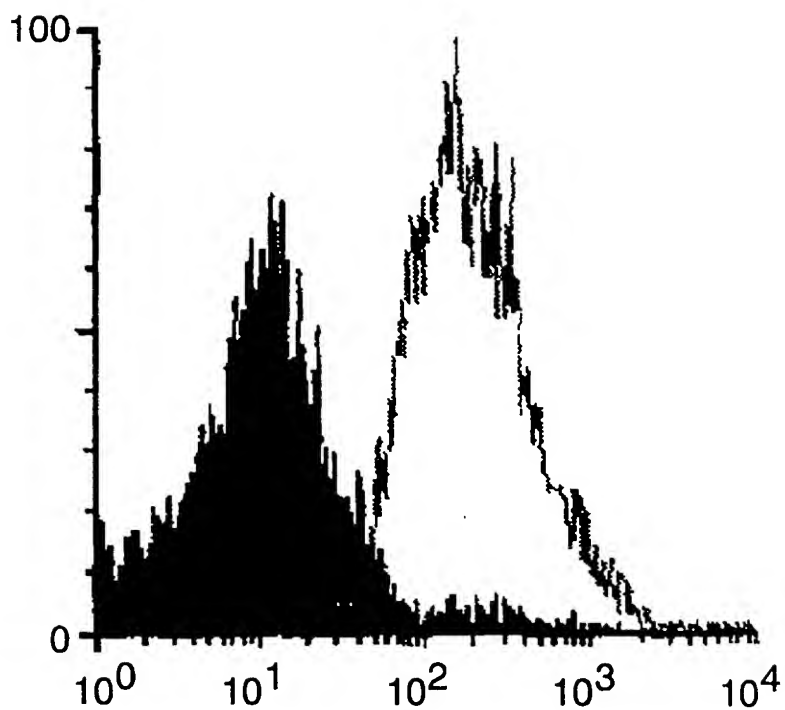
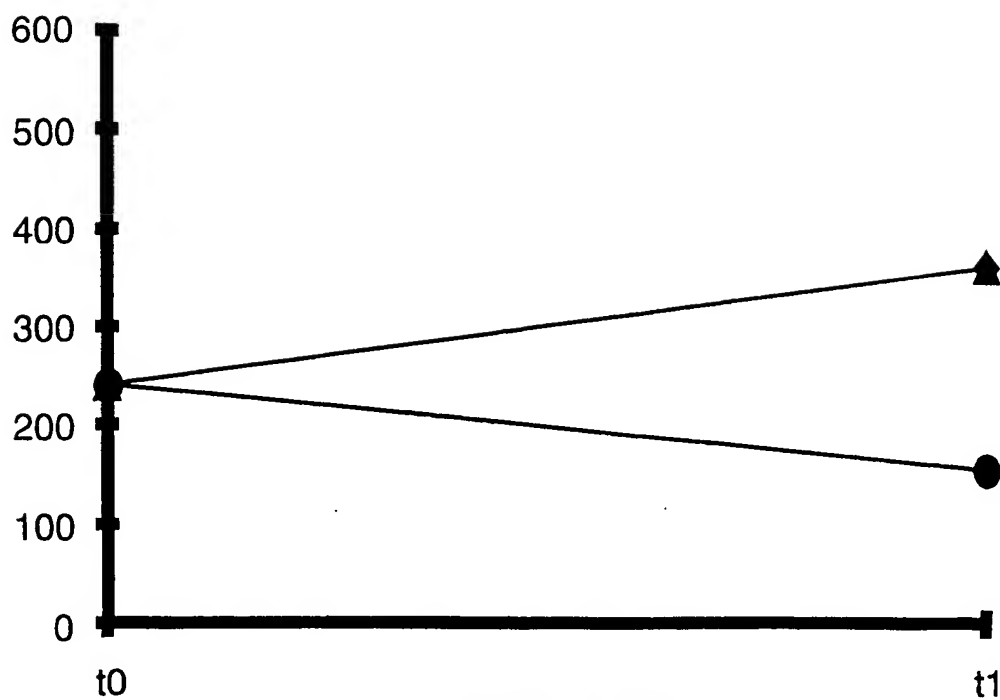
1. A protein comprising an amino acid sequence selected from the group consisting of SEQ IDs 2, 4, and 6.
2. A nucleic acid molecule which encodes a protein according to claim 1.
- 5 3. A nucleic acid molecule according to claim 2, comprising a nucleotide sequence selected from the group consisting of SEQ IDs 1, 3, and 5.
4. A protein comprising an amino acid sequence selected from the group consisting of SEQ IDs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, and 90.
- 10 5. A protein having 50% or greater sequence identity to a protein according to claim 4.
6. A protein comprising a fragment of an amino acid sequence selected from the group consisting of SEQ IDs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, and 90.
7. An antibody which binds to a protein according to any one of claims 4 to 6.
- 15 8. A nucleic acid molecule which encodes a protein according to any one of claims 4 to 6.
9. A nucleic acid molecule according to claim 8, comprising a nucleotide sequence selected from the group consisting of SEQ IDs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, and 89.
- 20 10. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of SEQ IDs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, and 89.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to any one of claims 8 to 10.

12. A nucleic acid molecule comprising a nucleotide sequences having 50% or greater sequence identity to a nucleic acid molecule according to any one of claims 8 to 11.
13. A nucleic acid molecule which can hybridise to a nucleic acid molecule according to any one of claims 8 to 12 under high stringency conditions.
- 5 14. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
15. A composition according to claim 14 being a vaccine composition or a diagnostic composition.
16. A composition according to claim 14 or claim 15 for use as a pharmaceutical.
- 10 17. The use of a composition according to claim 14 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria, particularly *Neisseria meningitidis*.

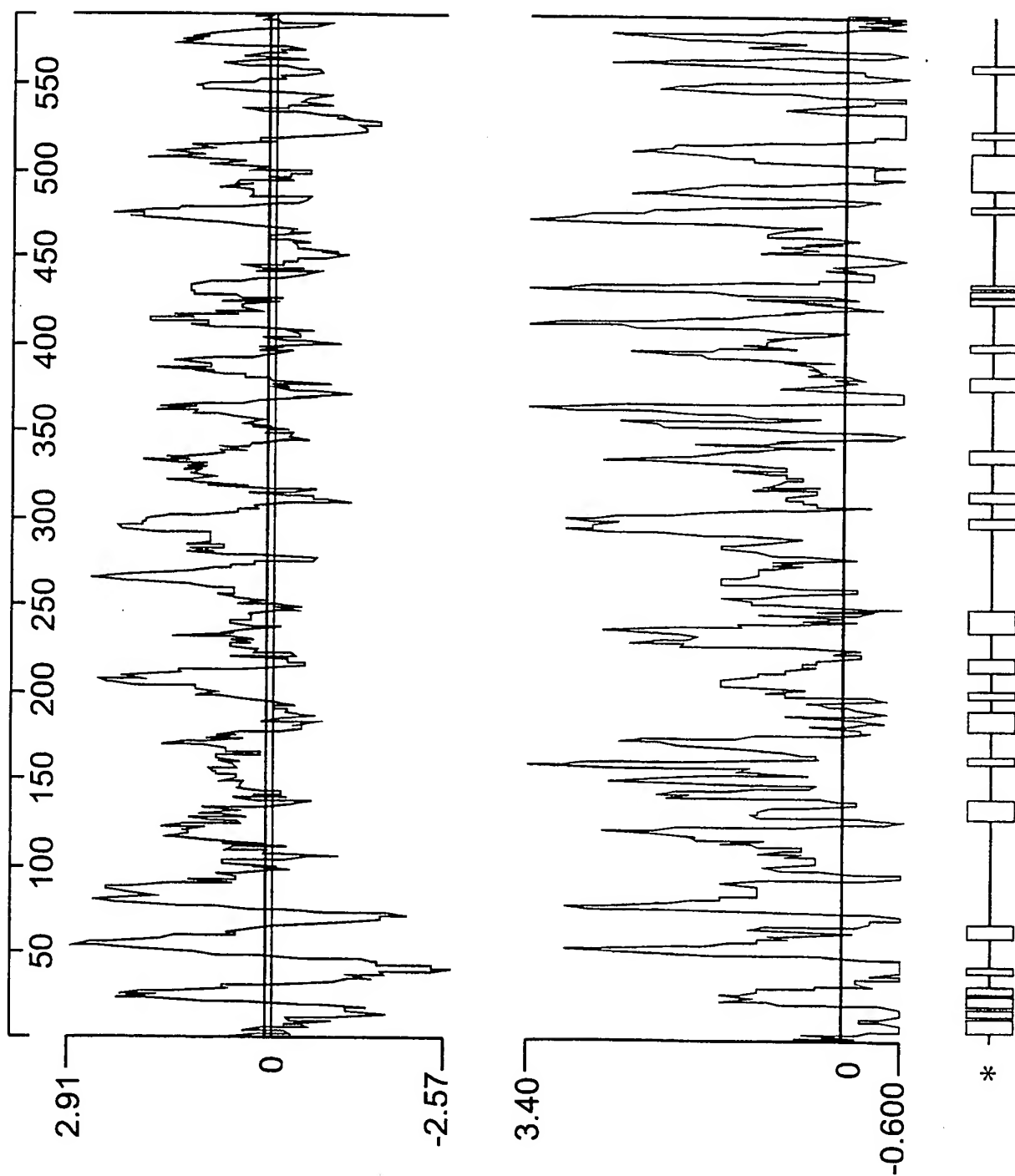
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FIG. 1A**FIG. 1B****FIG. 4A**

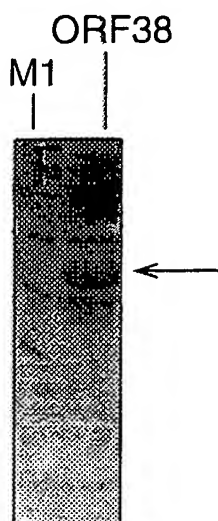
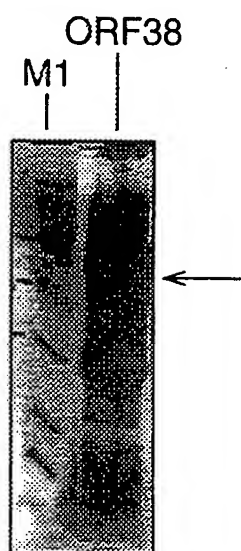
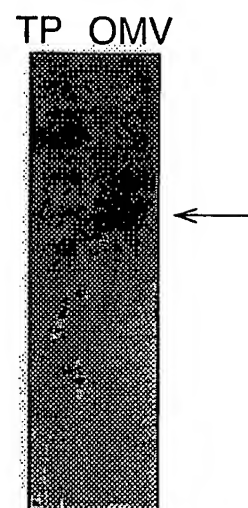
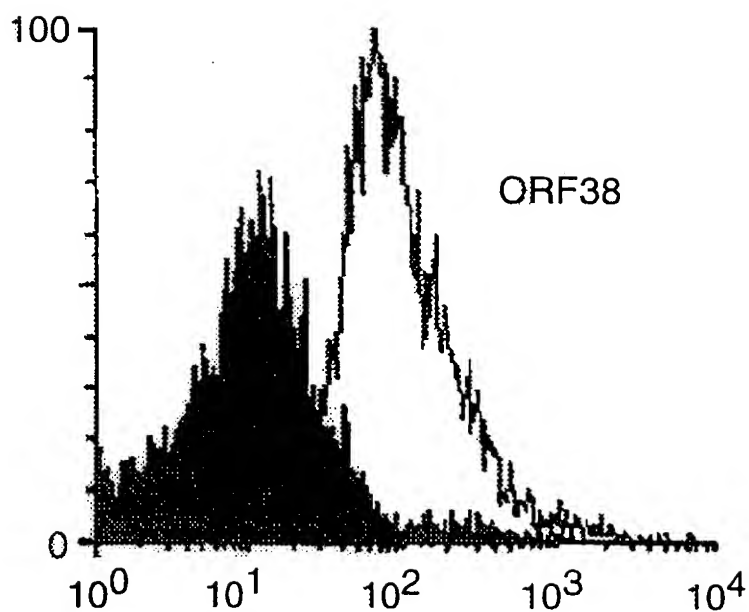
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**FIG. 1C****FIG. 1D**

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FIG. 2A**FIG. 2B****FIG. 2C****FIG. 2D**

• • •



FIG. 2E

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FIG. 3A

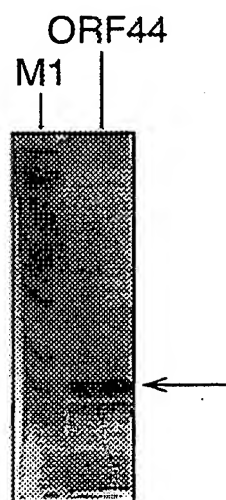


FIG. 3B

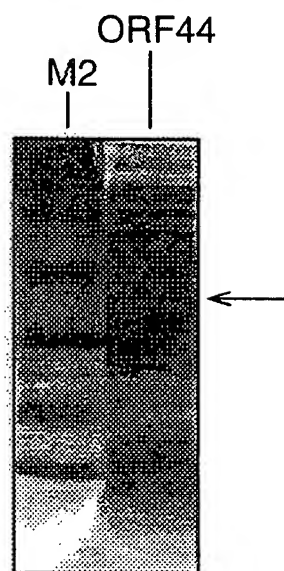
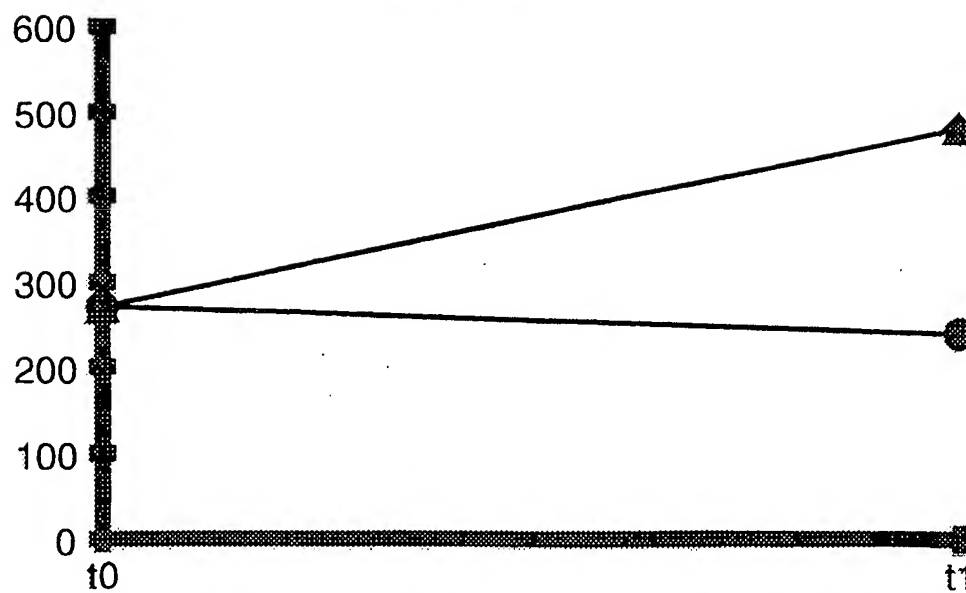
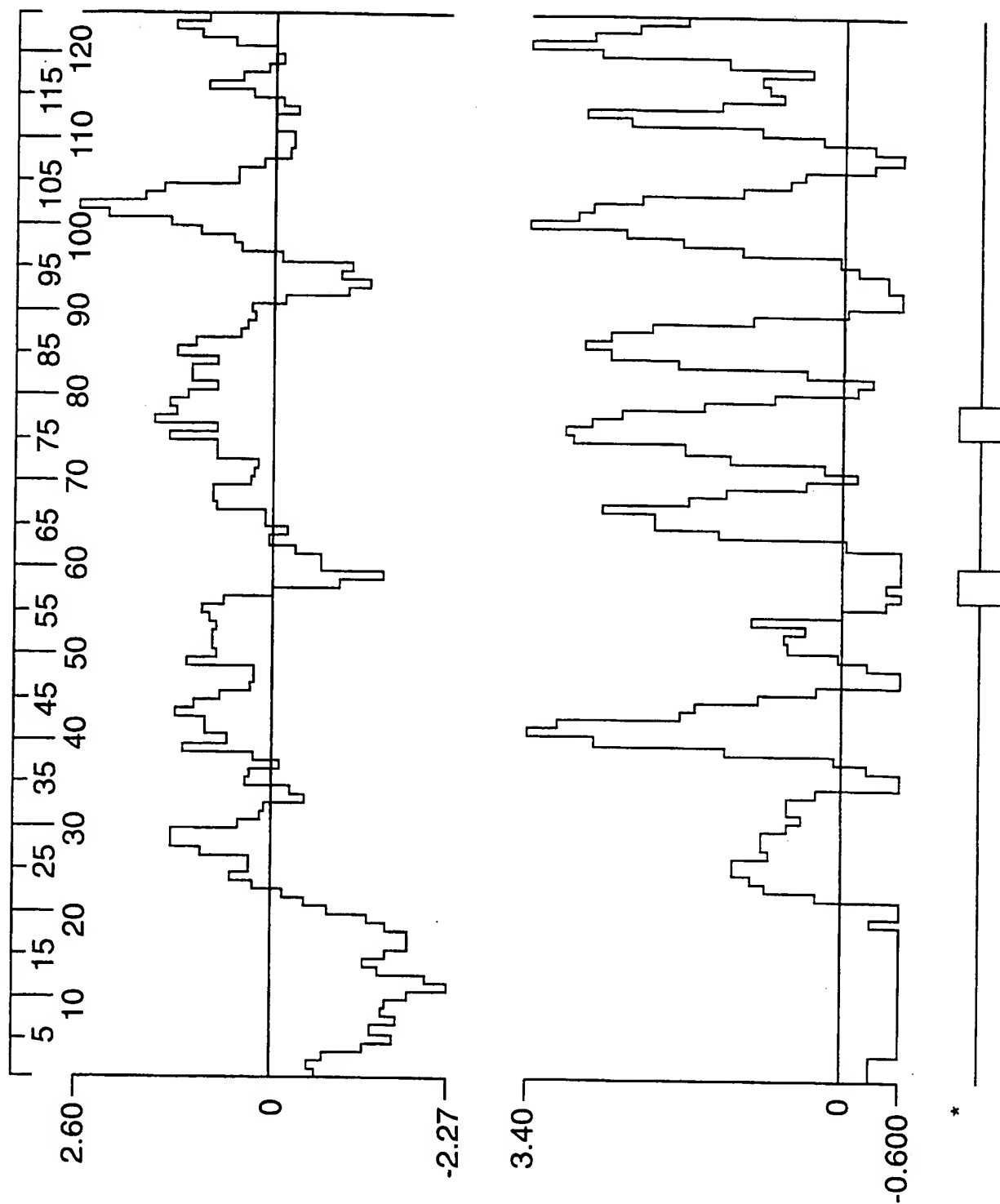


FIG. 3C

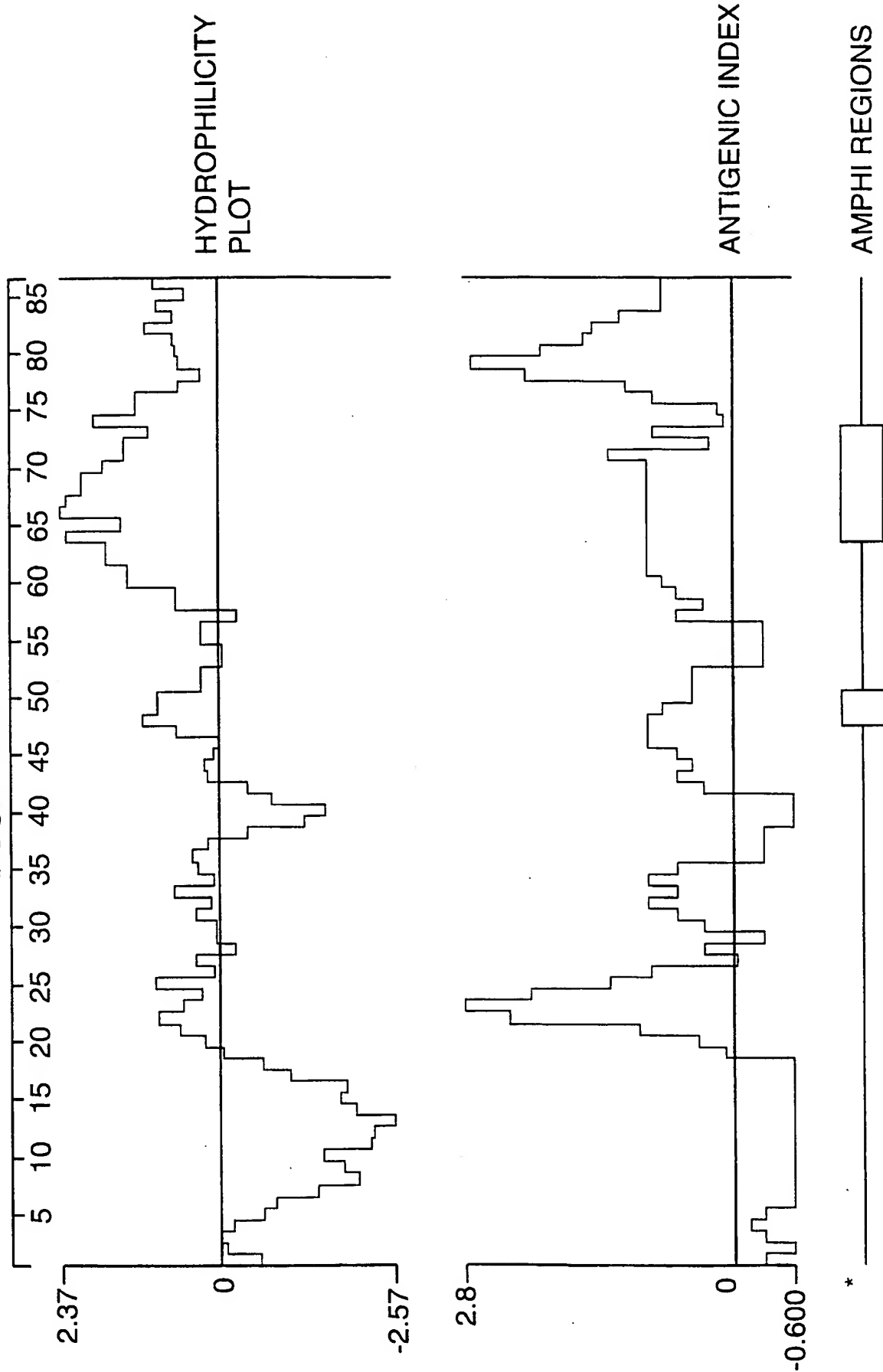


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**FIG. 3D**

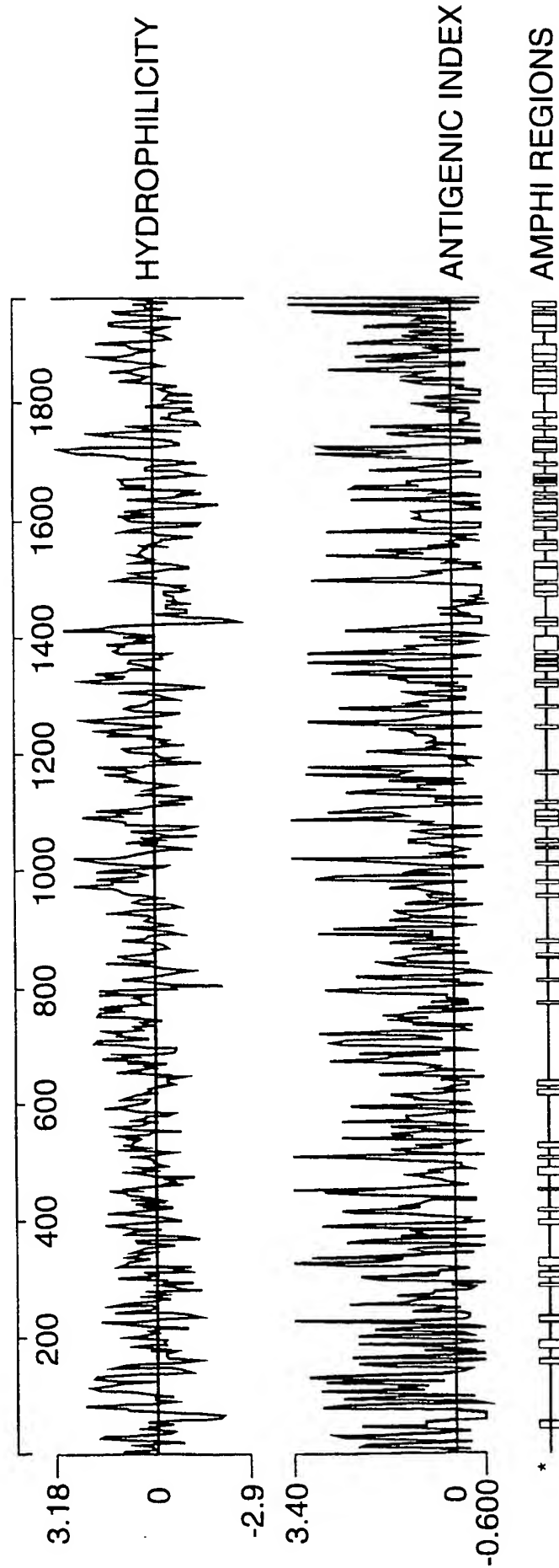
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FIG. 4B



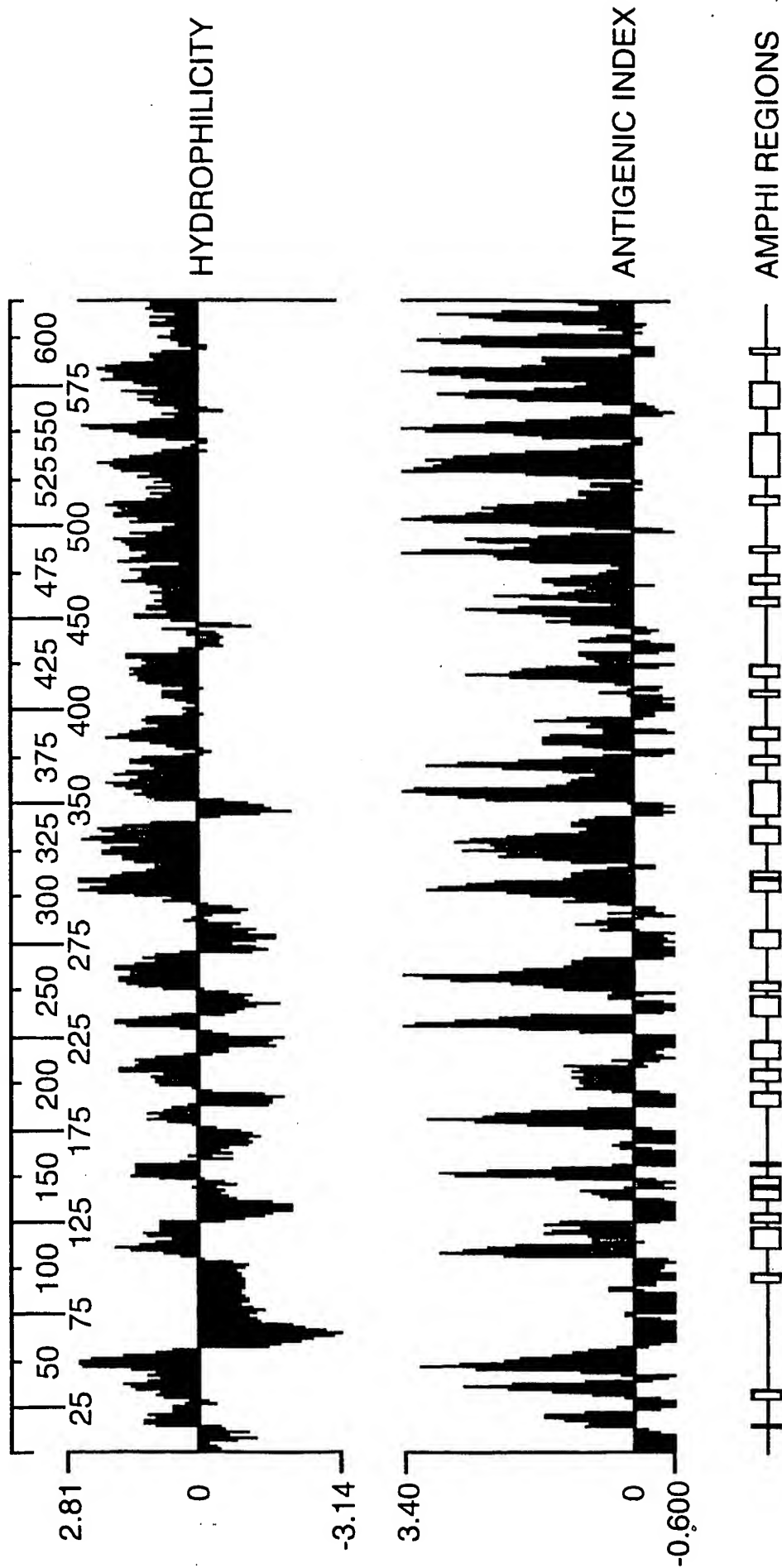
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FIG. 5



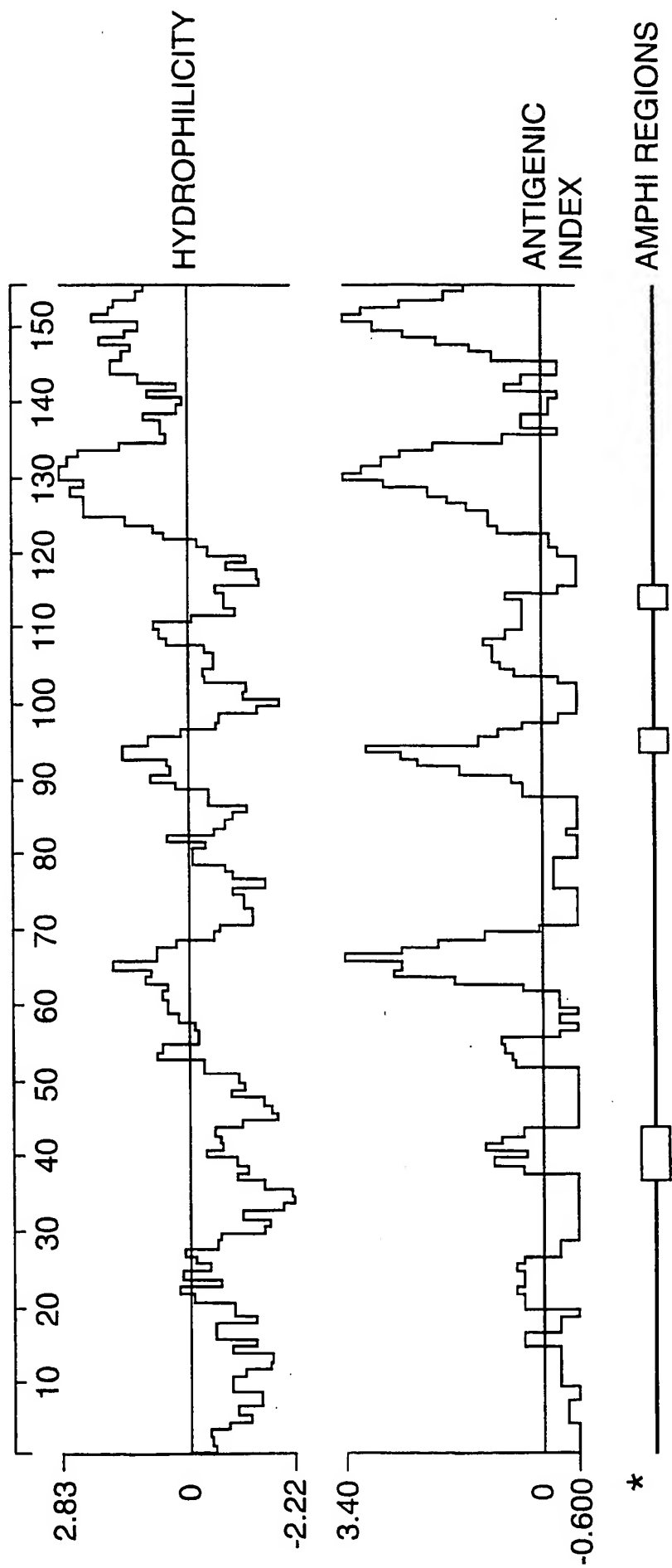
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FIG. 6



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FIG. 7



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